

# FIGURE 1

## Human DNase I

LOCUS HUMDNASEI 1039 bp mRNA PRI 06-MAR-1995  
 DEFINITION Human DNase I mRNA, complete cds.  
 ACCESSION M55983  
 VERSION M55983.1 GI:181623  
 KEYWORDS DNase I.  
 SOURCE Human pancreas, cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1039)  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672

FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="hDNase-18-1"  
 /tissue\_type="pancreas"  
 sig peptide 160..225  
 /gene="DNase I"  
 CDS 160..1008  
 /gene="DNase I"  
 /codon\_start=1  
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 /protein\_id="AAA63170.1"  
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 SYIVQILSRDYDIALVQEVDRDShLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERY  
 LFVYRPDQVSAVDSYYYDDGCEPCGNDFNREPAIVRFFSRFTEVREFAIVPLHAAPG  
 DAVAEIDALYDVYLDVQEKWGLEDMMLMGDFNAGCSYVRPSQWSSIRLWTSPTFWLI  
 PDSADTTATPTHCAIDRIVVAGMLLRGAVVPDSALPFNFQAAAYGLSDQLAQAI SDHYP  
 VEVMLK"  
 gene 160..1008  
 /gene="DNase I"  
 mat peptide 226..1005  
 /gene="DNase I"  
 /product="DNase I"

BASE COUNT 226 a 305 c 282 g 226 t  
 ORIGIN

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61 ttttctttta gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag
121 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg
181 ggggcgctgc tggcactggc ggccctactg cagggggccg tgccctgaa gatcgagcc
241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
301 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg
361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctactactac
421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
541 aacgacacct tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc
601 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgtcatgttg
721 atgggcgact tcaatgcggg ctgcagctat gtgagacct cccagtggtc atccatccgc
781 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca
841 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgcggtt
901 gttcccgact cggctcttcc ctttaacttc caggctgctt atggcctgag tgaccaactg
961 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agccctctcc
1021 cacaccagtt gaactgcag
```

//

# FIGURE 2

# human DNase I cDNA

(A)

LOCUS MHDNASE.DN 763 bp mRNA PRI 06-MAR-1995  
 DEFINITION Human DNase I mRNA, complete cds, Mature sequence modified to remove NarI site  
 ACCESSION M55963  
 NID q181623  
 KEYWORDS DNase I.  
 SOURCE Human pancreas, cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1039)  
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 FEATURES  
 source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="hDNase-18-1"  
 /tissue\_type="pancreas"  
 sig\_peptide 160..225  
 /gene="DNase I"  
 CDS 160..1008  
 /gene="DNase I"  
 /codon\_start=1  
 /product="DNase I"  
 /db\_xref="FID:q181624"  
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 PCGNITFNREPAIVRFFSPFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGL  
 EDVMLMGDFENAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG  
 MLLRGAVVPDSALFFNEQAAYGLSDQIAQAISDHYPVEVM,K"  
 gene 160..1008  
 /gene="DNase I"  
 mat\_peptide 226..1005  
 /gene="DNase I"  
 /product="DNase I"  
 BASE COUNT 168 a 236 c 220 g 159 t  
 ORIGIN

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1  CTGAAGATCG  CAGCCTTCAA  CATCCAGACA  TTTGGGGAGA  CCAAGATGTC  CAATGCCACC
61  CTCGTCAGCI  ACATTGTGCA  GATCCTGAGC  CGCTACGACA  TCGCCCTGGT  CCAGGAGGTC
121  AGAGACAGCC  ACCTGACTGC  CGTGGGGAAG  CTGCTGGACA  ACCTCAATCA  GGACGCACCA
181  GACACCTATC  ACTACGTGGT  CAGTCAGCCA  CTGGGACGGA  ACAGCTATAA  GGAGCGCTAC
241  CTGTTCTGT  ACAGGCCTGA  CCAGGTGTCT  GCGGTGGACA  GCTACTACTA  CGATGATGGC
301  TCGGAGCCCT  GCGGGAACGA  CACCTTCAAC  CGAGAGCCAG  CCATTGTTCAG  GTTCTTCTCC
361  CGGTTCACAG  AGGTCAGGGA  GTTGGCCATT  GTTCCCTGTC  ATGCGGCCCC  GGGGACGCA
421  GTAGCCGAGA  TCGACGCTCI  CTATGACGTC  TACCTGGATG  TCCAAGAGAA  ATGGGGCTTG
481  GAGGACGTCA  TGTGTATGGG  CGACTTCAAT  GCGGGCTGCA  GCTATGTGAG  ACCCTCCCAG
541  TGGTCATCCA  TCCGCTGTGT  GACAAGCCCC  ACCCTCCAGT  GGCTGATCCC  CGACAGCGCT
601  GACACCCACG  CTACCCACAC  GCAGTGTGCC  TAIGACAGGA  TCGTGGTTGC  AGGGATGCTG
661  CCCCCAGGGG  CCGTGTGTCC  CGACTCGGCT  CTTCCTTTTA  ACTTCCAGGC  TGCCTATGGC
721  CTGAGTGACC  AACTGGCCCA  AGCCATCAGT  GACCACTATC  CAGTGGAGGT  GATGCTGAAG
781  TGA

```

//

# FIGURE 2(B)

LOCUS PAS155\_GB. 858 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

Location/Qualifiers

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/note="160 to 225 of Untitled1"

frag <10..>75

/note="1 to 1039 of M55983.DNA [Split]"

source <10..>75

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="hDNase-18-1"

/tissue\_type="pancreas [Split]"

sig\_peptide 10..75

/gene="DNase I"

CDS 10..>75

/gene="DNase I"

/codon\_start="1"

/product="DNase I"

/db\_xref="PID:g181624"

/translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV  
SYIVQILSRDYDIALVQEVDRDShLTAVGKLLDNLNQDAPDPTYHYVVSEPLGRNSYKERY  
LFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG  
D... [Split]"

gene 10..>75

/gene="DNase I [Split]"

frag 76..858

/note="1 to 783 of mod humanDNaseI"

frag 76..858

/note="1 to 72 of 104linker"

frag join(76..>129,<131..147)

/note="1 to 72 of 103linker [Split]"

frag join(76..>126,<127..>129,<131..147)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 177 A 260 C 251 G 170 T 0 OTHER

ORIGIN -

1 GGCGCCACCA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC GGCCCTACTG

61 CAGGGGGCCG TGTCCTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG

121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC

181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC

241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC

301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC

361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT

421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG

481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA

541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT

601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG

661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG

721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC

781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG

841 GAGGTGATGC TGAAGTGA

FIGURE 3

(A) pAS6 - light chain

LOCUS HMFG1LC2.D 721 bp DNA  
 DEFINITION HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER.  
 ACCESSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE 1 (BASES 1 TO 342)  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 ETC  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT SCANNED IN FROM JOURNAL  
 FEATURES  
 SITES

This is the sequence of the HMFG1 light chain gene with the Vnp leader sequence attached. Translate from residue 1. Note residue 399 is T > A in all clones leading to R133 silent mutation (T in Verhoeyen paper)

BASE COUNT 197 a 202 c 182 g 140 t  
 ORIGIN ?

LEADER SEQ  
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCGAC  
 61 ATCCAGATGA CCCAGAGCCC AAGCAGCCTG AGCGCCAGCG TGGGTGACAG AGTGACCATC  
 121 ACCTGTAAGT CCAGTCAGAG CCTTTTATAT AGTAGCAATC AAAAGATCTA CTTGGCCTGG  
 181 TACCAGCAGA AGCCAGGTAA GGCTCCAAAG CTGCTGATCT ACTGGGCATC CACTAGGGAA  
 241 TCTGGTGTGC CAAGCAGATT CAGCGGTAGC GGTAGCGGTA CCGACTTCAC CTTCACCATC  
 301 AGCAGCCTCC AGCCAGAGCA CATCGCCACC TACTACTGCC AGCAATATTA TAGATATCCT  
 361 CGGACGTTGG GCCAAGGGAC CAAGGTGGAA ATCAACGAA CTGTGGCTGC ACCATCTGTC  
 421 TTCATCTTCC CGCCATCTGA TGAGCAGTIG AAATCTGGAA CTGCCTCTGT TGTGTGCTG  
 481 CTGAATAACT TCTATCCAG AGAGGCCAAN GTACAGTGGG AGGTGGATAA CGCCCTCCAA  
 541 TCGGGTAACT CCCAGGAGAG TGTCACAGAG CAGGACAGCA AGGACAGCAC CTACAGCCTC  
 601 AGCAGCACCC TGACGCTGAG CAAAGCAGAC TACGAGAAAC ACAAGTCTA CGCCTGCGAA  
 661 GTCACCCATC AGGGCCTGAG CTCGCCCGTC ACAAAGAGCT TCAACAGGGG AGAGTGTTAG  
 721 A

//

# Figure 3(B)

LOCUS HHMFG1KLC\_ 730 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
 frag 10..730  
 /note="1 to 721 of hHMFG1light chain"  
 frag 10..730  
 /note="1 to 72 of 104linker"  
 frag join(10..>63,<65..81)  
 /note="1 to 72 of 103linker [Split]"  
 frag join(10..>60,<61..>63,<65..81)  
 /note="1 to 78 of 102linker [Split]"

BASE COUNT 198 A 208 C 184 G 140 T 0 OTHER  
 ORIGIN -

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1  GCGGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA
121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTATATA GTAGCAATCA AAAGATCTAC
181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC
241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC
301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT
361 AGATATCCTC GGACGTTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA
421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT
481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
721 GAGTGTTAGA

```

//

500  
 600

Figure 3 (c)

HMFG-1 light chain with Vnp Leader (shaded)

MCWSCIIIELVATATGMHSDIQMTQSPSSLSASVGDRVITITCKSSQSL  
LYSSNQKIYLA WYQQKPGKAPKLLIYWASTRESGVPSRFSGSGSGT  
DFTFTISLQPEDATYYCQQYYRYPRTFGQGTKVEIKRTVAAPSVFI  
FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV  
TEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN  
RGEC

FIGURE 3

(D) PAS6 - heavy chain

LOCUS HMMFG1HC.D 1404 bp DNA  
 DEFINITION HUMANISED HMMFG1 heavy chain  
 ACCESSION HMMFG1H  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT VH domain SCANNED IN FROM JOURNAL  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 SITES Note  
 BASE COUNT 333 a 439 c 379 g 253 t  
 ORIGIN

← LINKER →

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAGGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATC TAGATACAAT
241 GAGAAGTICA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TCAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGCTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCTTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACTCA
541 GGGGCCCTGA CCAGCGCGGT GCACACCTTC CCGGCTGTCC TACAGTCTAC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTCCCTTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCA GCACCTGAA TCCTGGGGGG ACCGTCAGTC
781 TTCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCAAC
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGGTGGAGG TGCATAATGC CAAAGCAAAG CCGCGGGAGG AGCAGTACAA CAGCAGGTAC
961 CGTGTGGTCA GCGTCTCTAC CGTCTGTGAC CAGGACTGGC TGATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTGCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCAAC GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAA GGCCTCTATC CCAGCGACAT CGCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCCTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCRGAGAGGC
1381 CTCTCCCTGT CTCCGGGTAA ATGA
  
```

Antibody DNAe Fusions made HERE (eg PAS 34-39.)

End of lower hinge region of HEAVY CHAIN. PAPE Amino  
 Acid Seq. Fab<sub>2</sub> fusions were made at this point.

Those with HYBRID HINGES ARE ALTERED FURTHER  
 UP

ie.

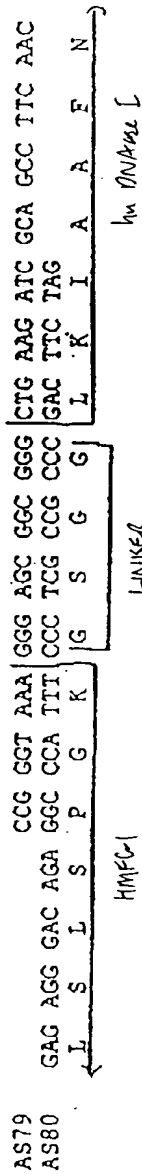
THIS PART GACAAAAAACTGACACA  
 IS → D K T H T

AFTER THIS SEQUENCE YOU GET THE  
 HYBRID HINGE + LINKER SEQUENCES

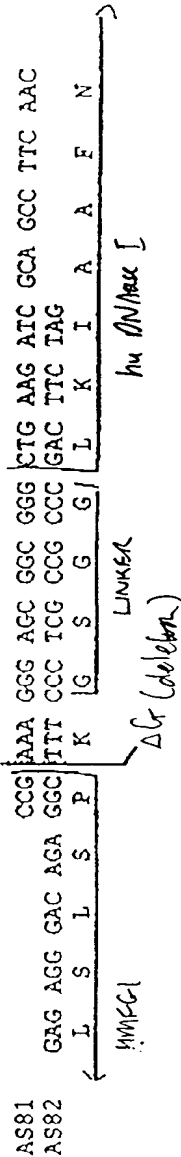
Then DNase I (eg Fab-DNAe construct PAS302)

(A.) Oligos involved in the fusion of whole antibody-DNAse

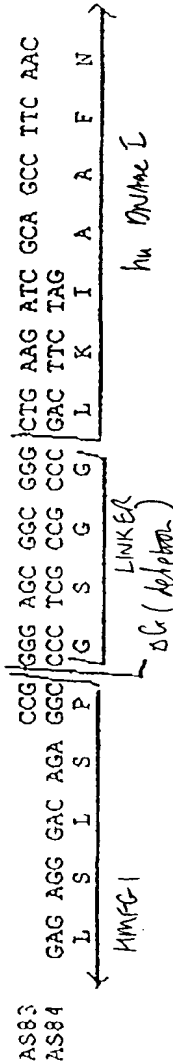
Constructs pAS34/37



Constructs pAS35/38

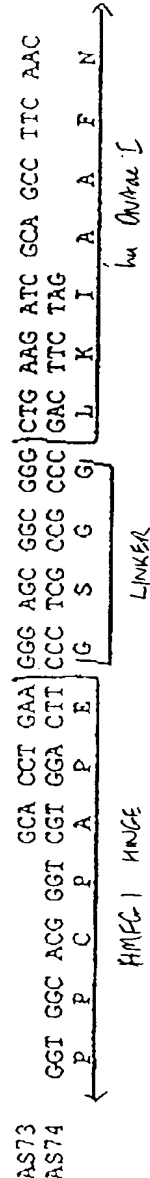


Constructs pAS36/39



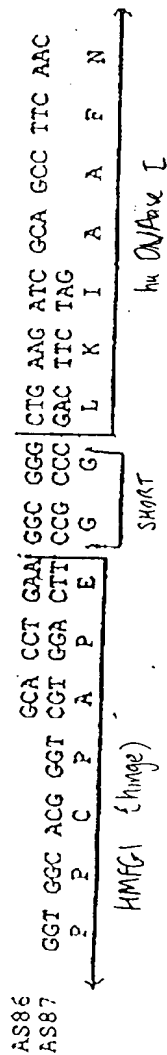
Oligos involved in the fusion of Fab'2-DNaseI

Constructs pAS23/27

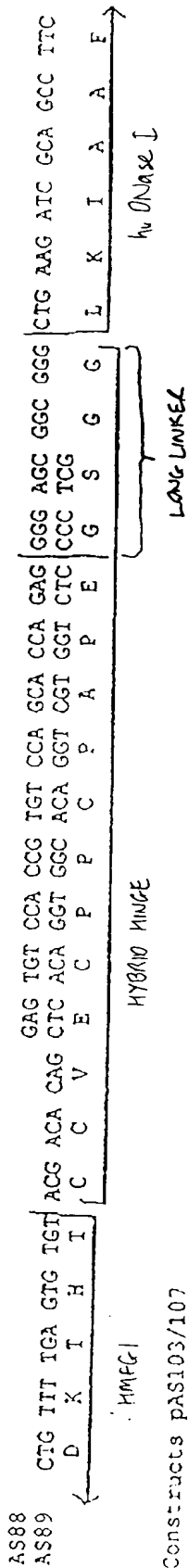


(B.) Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

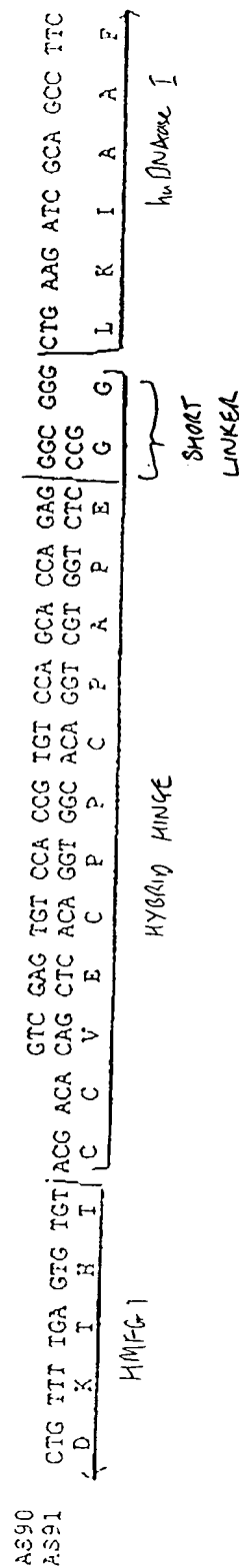
Constructs PAS101/105



Constructs PAS102/106



Constructs PAS103/107



(A) pAS23

LOCUS PAS23.DNA 1554 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 344 a 468 c 434 g 308 t  
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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAG GGAGCGGCGG GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAG ATTTGGGGAG ACCAAGATGT CCAATGCCAC CTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTTCGTG
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCCTTCTC CCGGTTTACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCTCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCTGTG GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGTTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGAGG TGATGCTGAA GTGA

```

//

# Figure 5(B)

LOCUS FDDNASE23\_ 1554 BP SS-DNA SYN 25-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -  
 FEATURES Location/Qualifiers  
   frag join(1..>720,<787..1554)  
     /note="1 to 1554 of 23.dna [Split]"  
   frag 721..786  
     /note="1 to 66 of 23/27linker"  
   frag join(721..>735,<736..786)  
     /note="1 to 78 of 102linker [Split]"  
 BASE COUNT 344 A 466 C 435 G 309 T 0 OTHER  
 ORIGIN -

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1  ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61  GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGAATACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCGG GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCTGT
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTTACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCTTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCTGTG GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGTTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
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# Figure S(c)

LOCUS FDDNASE23K 1563 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
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 /note="1 to 1554 of 23.dna [Split]"  
 frag 730..795  
 /note="1 to 66 of 23/27linker"  
 frag join(730..>744,<745..795)  
 /note="1 to 78 of 102linker [Split]"  
 BASE COUNT 345 A 472 C 437 G 309 T 0 OTHER  
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121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG
541 TGGAAGTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA
601 GGAAGTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
841 CTCGTAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
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1141 CGGTTACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGACGCA
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1321 TGGTCATCCA TCCGCCGTGT GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
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File : PAS23.DNA  
 Range : 1 - 1554 Mode : Normal  
 Codon Table : UniProt

FIGURE 5(D)

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	M G W S C I I L F L V A T A T G V H					
	63	72	81	90	99	108
	TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA					
	S Q V Q L V Q S G A E V K K P G A S					
	117	126	135	144	153	162
	GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG					
	V K V S C K A S G Y T F S A Y W I E					
	171	180	189	198	207	216
	TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT					
	W V R Q A P G K G L E W V G E I L P					
	225	234	243	252	261	270
	GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT					
	G S N N S R Y N E K F K G R V T V T					
	279	288	297	306	315	324
	AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG					
	R D T S T N T A Y M E L S S L R S E					
	333	342	351	360	369	378
	GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC					
	D T A V Y Y C A R S Y D F A W F A Y					
	387	396	405	414	423	432
	TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG					
	W G Q G T L V T V S S A S T K G P S					
	441	450	459	468	477	486
	GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG					
	V F P L A P S S K S T S G G T A A L					
	495	504	513	522	531	540
	GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA					
	G C L V K D Y F P E P V T V S W N S					
	549	558	567	576	585	594
	GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA					
	G A L T S G V H T F P A V L Q S S G					

603	612	621	630	639	648
CTC TAC TCC CTC AGC	AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG				
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG					
E G S G G L K I A A F N I Q T F G E					
819	828	837	846	855	864
ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC					
T K M S N A T L V S Y I V Q I L S R					
873	882	891	900	909	918
TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG					
Y D I A L V Q E V R D S H L T A V G					
927	936	945	954	963	972
AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC					
K L L D N L N Q D A P D T Y H Y V V					
981	990	999	1008	1017	1026
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S E P L G R N S Y K E R Y L F V Y R					
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CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC					
P D Q V S A V D S Y Y Y D D G C E P					
1089	1098	1107	1116	1125	1134
TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG					
C G N D T F N R E P A I V R F F S R					
1143	1152	1161	1170	1179	1188
TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC					
F T E V R E F A I V P L H A A P G D					
1197	1206	1215	1224	1233	1242

GCA	GTA	GCC	GAC		GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG		GTC	CAA	GAG	AAA
-----																	
A	V	A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K
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1251				1260			1269			1278			1287			1296	
TGG	GGC	TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT
-----																	
W	G	L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y
-----																	
1305				1314			1323			1332			1341			1350	
GTG	AGA	CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG
-----																	
V	R	P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q
-----																	
1359				1368			1377			1386			1395			1404	
TGG	CTG	ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT
-----																	
W	L	I	P	D	S	A	D	T	T	A	T	P	T	H	C	A	Y
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1413				1422			1431			1440			1449			1458	
GAC	AGG	ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG
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D	R	I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S
-----																	
1467				1476			1485			1494			1503			1512	
GCT	CTT	CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA
-----																	
A	L	P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q
-----																	
1521				1530			1539			1548							
GCC	ATC	AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'			
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A	I	S	D	H	Y	P	V	E	V	M	L	K	*				

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LOCUS PAS27.DNA 1584 bp mRNA PRI 06-MAR-1995  
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 ACCESSION  
 NID  
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 SOURCE DNase I sequence is from assembled oligos (thus modified c/f MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 354 a 474 c 446 g 310 t  
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LOCUS FDDNASE27\_ 1584 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

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661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT  
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781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC  
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC  
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT  
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG  
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC  
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1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGACGC AGTAGCCGAG  
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC  
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC  
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA  
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG  
1441 GCCGTTGTTT CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC  
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1561 CCCAAAAAGA AGCGCAAGGT TTGA

FOCUS FDDNASE27K 1593 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -  
 FEATURES Location/Qualifiers  
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         /note="1 to 1584 of 27.dna [Split]"  
     frag 730..795  
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         /note="1 to 78 of 102linker [Split]"  
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     181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT  
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     301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA  
     361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA  
     421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG  
     481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCAGG GACGGTGTCG  
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     601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC  
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     781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC  
     841 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC  
     901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA  
     961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC  
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     1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG  
     1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCCAG  
     1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT  
     1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG  
     1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC  
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File : PAS27.DNA  
Range : 1 - 584 Mode : Normal  
Codon Table : Universal

EXE 6(D)

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-----
      63      72      81      90      99      108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
   S  Q  V  Q  L  V  Q  S  G  A  E  V  K  K  P  G  A  S
-----
     117     126     135     144     153     162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
   V  K  V  S  C  K  A  S  G  Y  T  F  S  A  Y  W  I  E
-----
     171     180     189     198     207     216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
   W  V  R  Q  A  P  G  K  G  L  E  W  V  G  E  I  L  P
-----
     225     234     243     252     261     270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
   G  S  N  N  S  R  Y  N  E  K  F  K  G  R  V  T  V  T
-----
     279     288     297     306     315     324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
   R  D  T  S  T  N  T  A  Y  M  E  L  S  S  L  R  S  E
-----
     333     342     351     360     369     378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
   D  T  A  V  Y  Y  C  A  R  S  Y  D  F  A  W  F  A  Y
-----
     387     396     405     414     423     432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
   W  G  Q  G  T  L  V  T  V  S  S  A  S  T  K  G  P  S
-----
     441     450     459     468     477     486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
   V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L
-----
     495     504     513     522     531     540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
   G  C  L  V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S
-----
     549     558     567     576     585     594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
   G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G
-----

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- 1 -

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC TCC TTG GGC ACC CAG					
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGG AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG					
E G S G G L K I A A F N I Q T F G E					
819	828	837	846	855	864
ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC					
T K M S N A T L V S Y I V Q I L S R					
873	882	891	900	909	918
TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG					
Y D I A L V Q E V R D S H L T A V G					
927	936	945	954	963	972
AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC					
K L L D N L N Q D A P D T Y H Y V V					
981	990	999	1008	1017	1026
AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG					
S E P L G R N S Y K E R Y L F V Y R					
1035	1044	1053	1062	1071	1080
CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC					
P D Q V S A V D S Y Y Y D D G C E P					
1089	1098	1107	1116	1125	1134
TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTG AGG TTC TTC TCC CGG					
C G N D T F N R E P A I V R F F S R					
1143	1152	1161	1170	1179	1188
TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC					
F T E V R E F A I V P L H A A P G D					
1197	1206	1215	1224	1233	1242

GCA	GTA	GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA	GAG	AAA
A	V	A	E		D	A	L	Y	D	V	Y	L		V	Q	E	K

1251	1260	1269	1278	1287	1296
TGG	GGC	TTG	GAG	GAC	GTC
ATG	TTG	ATG	GGC	GAC	TTC
AAT	GCG	GGC	TGC	AGC	TAT
W	G	L	E	D	V
M	L	M	G	D	F
N	A	G	C	S	Y

1305	1314	1323	1332	1341	1350
GTG	AGA	CCC	TCC	CAG	TGG
TCA	TCC	ATC	CGC	CTG	TGG
ACA	AGC	CCC	ACC	TTC	CAG
V	R	P	S	Q	W
S	S	I	R	L	W
T	S	P	T	F	Q

1359	1368	1377	1386	1395	1404
TGG	CTG	ATC	CCC	GAC	AGC
GCT	GAC	ACC	ACA	GCT	ACA
CCC	ACG	CAC	TGT	GCC	TAT
W	L	I	P	D	S
A	D	T	T	A	T
P	T	H	C	A	Y

1413	1422	1431	1440	1449	1458
GAC	AGG	ATC	GTG	GTT	GCA
GGG	ATG	CTG	CTC	CGA	GGG
GCC	GTT	GTT	CCC	GAC	TCG
D	R	I	V	V	A
G	M	L	L	R	G
A	V	V	P	D	S

1467	1476	1485	1494	1503	1512
GCT	CTT	CCC	TTT	AAC	TTC
CAG	GCT	GCC	TAT	GGC	CTG
AGT	GAC	CAA	CTG	GCC	CAA
A	L	P	F	N	F
Q	A	A	Y	G	L
S	D	Q	L	A	Q

1521	1530	1539	1548	1557	1566
GCC	ATC	AGT	GAC	CAC	TAT
CCA	GTG	GAG	GTG	ATG	CTG
AAG	GGG	GGC	GGA	CCC	AAA
A	I	S	D	H	Y
P	V	E	V	M	L
K	<u>G</u>	<u>G</u>	<u>G</u>	<u>P</u>	<u>K</u>

1575	1584
AAG	AAG
CGC	AAG
GTT	TGA
3'	
K	K
R	K
V	*

FIGURE 7

(A) pAS34

LOCUS PAS34.DNA 2196 bp 2196 bp 2196 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 34  
 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file)  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS79 and AS80  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 SITES Note  
 BASE COUNT 501 a 677 c 607 g 411 t  
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAG CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAAC TACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAATC
781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAA TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCAGTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCG TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCAGAGAG CAGCCATTGT CAGGTTCTTC TCCCGTTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCAGACAG GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAAGTTCCA GGCTGCCTAT GGCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

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File : PAS34.DNA  
 Range : 1 - 2196 Mode : Normal  
 Codon Table : UniProt

FIGURE 7(B)

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      9      18      27      36      45      54
5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC
   M  G  W  S  C  I  I  L  F  L  V  A  T  A  T  G  V  H
-----
      63      72      81      90      99      108
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA
   S  Q  V  Q  L  V  Q  S  G  A  E  V  K  K  P  G  A  S
-----
      117      126      135      144      153      162
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG
   V  K  V  S  C  K  A  S  G  Y  T  F  S  A  Y  W  I  E
-----
      171      180      189      198      207      216
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT
   W  V  R  Q  A  P  G  K  G  L  E  W  V  G  E  I  L  P
-----
      225      234      243      252      261      270
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT
   G  S  N  N  S  R  Y  N  E  K  F  K  G  R  V  T  V  T
-----
      279      288      297      306      315      324
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG
   R  D  T  S  T  N  T  A  Y  M  E  L  S  S  L  R  S  E
-----
      333      342      351      360      369      378
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC
   D  T  A  V  Y  Y  C  A  R  S  Y  D  F  A  W  F  A  Y
-----
      387      396      405      414      423      432
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG
   W  G  Q  G  T  L  V  T  V  S  S  A  S  T  K  G  P  S
-----
      441      450      459      468      477      486
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG
   V  F  P  L  A  P  S  S  K  S  T  S  G  G  T  A  A  L
-----
      495      504      513      522      531      540
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA
   G  C  L  V  K  D  Y  F  P  E  P  V  T  V  S  W  N  S
-----
      549      558      567      576      585      594
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA
   G  A  L  T  S  G  V  H  T  F  P  A  V  L  Q  S  S  G
-----
      603      612      621      630      639      648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG
   L  Y  S  L  S  S  V  V  T  V  P  S  S  S  L  G  T  Q
-----
      657      666      675      684      693      702

```

ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA						
T	Y	I	C		V	N	H	K	P	S	N	T	K		D	K	K						
711				720				729				738				747				756			
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT						
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P						
765				774				783				792				801				810			
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC						
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T						
819				828				837				846				855				864			
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC						
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H						
873				882				891				900				909				918			
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT						
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N						
927				936				945				954				963				972			
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC						
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S						
981				990				999				1008				1017				1026			
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG						
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K						
1035				1044				1053				1062				1071				1080			
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA						
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K						
1089				1098				1107				1116				1125				1134			
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG						
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L						
1143				1152				1161				1170				1179				1188			
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC						
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D						
1197				1206				1215				1224				1233				1242			
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG						
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T						
1251				1260				1269				1278				1287				1296			
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG						
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V						
1305				1314				1323				1332				1341				1350			
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG						
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E						

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC	TAC ACG CAG AAG AGC CTC TCC CTG T	GGT AAA GGG			
A L H N	H Y T Q K S L S L S P G K	<u>G</u>			
1413	1422	1431	1440	1449	1458
AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
<u>S G G</u>	L K I A A F N I Q T F G E T K				
1467	1476	1485	1494	1503	1512
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
M S N A T L V S Y I V Q I L S R Y D					
1521	1530	1539	1548	1557	1566
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
I A L V Q E V R D S H L T A V G K L					
1575	1584	1593	1602	1611	1620
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
L D N L N Q D A P D T Y H Y V V S E					
1629	1638	1647	1656	1665	1674
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
P L G R N S Y K E R Y L F V Y R P D					
1683	1692	1701	1710	1719	1728
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
Q V S A V D S Y Y Y D D G C E P C G					
1737	1746	1755	1764	1773	1782
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA					
N D T F N R E P A I V R F F S R F T					
1791	1800	1809	1818	1827	1836
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
E V R E F A I V P L H A A P G D A V					
1845	1854	1863	1872	1881	1890
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC					
A E I D A L Y D V Y L D V Q E K W G					
1899	1908	1917	1926	1935	1944
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA					
L E D V M L M G D F N A G C S Y V R					
1953	1962	1971	1980	1989	1998
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG					
P S Q W S S I R L W T S P T F Q W L					
2007	2016	2025	2034	2043	2052
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG					
I P D S A D T T A T P T H C A Y D R					

2061      070      2079      2088      07      2106  
 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT  
 -----  
 I V V A G M L L R G A V V P D S A L  
  
 2115      2124      2133      2142      2151      2160  
 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC  
 -----  
 P F N F Q A A Y G L S D Q L A Q A I  
  
 2169      2178      2187      2196  
 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'  
 -----  
 S D H Y P V E V M L K \*

(A) pAS35

LOCUS PAS35.DNA 2193 bp 2193 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 35  
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS81 and AS82  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)  
 SITES Note  
 BASE COUNT 500 a 677 c 606 g 410 t  
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGCGCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCGTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTIONC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGAGAG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAAGGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCC GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTACAG AGGTCAGGGA GTTTGCCATT
1801 GTTCCCCCTG ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGAGGAT GATGCTGAAG TGA

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5'	9	18	27	36	45	54	
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC
TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT
GTC	CAC						
M	G	W	S	C	I	I	L
F	L	V	A	T	A	T	G
V	H						
63	72	81	90	99	108		
TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT
GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG
GCC	TCA						
S	Q	V	Q	L	V	Q	S
G	A	E	V	K	K	P	G
A	S						
117	126	135	144	153	162		
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT
GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG
ATA	GAG						
V	K	V	S	C	K	A	S
G	Y	T	F	S	A	Y	W
I	E						
171	180	189	198	207	216		
TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG
GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT
TTA	CCT						
W	V	R	Q	A	P	G	K
G	L	E	W	V	G	E	I
L	P						
225	234	243	252	261	270		
GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT
GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA
GTC	ACT						
G	S	N	N	S	R	Y	N
E	K	F	K	G	R	V	T
V	T	V	T				
279	288	297	306	315	324		
AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC
TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG
TCT	GAG						
R	D	T	S	T	N	T	A
Y	M	E	L	S	S	L	R
S	E						
333	342	351	360	369	378		
GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA
AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT
GCT	TAC						
D	T	A	V	Y	Y	C	A
R	S	Y	D	F	A	W	F
A	Y						
387	396	405	414	423	432		
TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA
GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC
CCA	TCG						
W	G	Q	G	T	L	V	T
V	S	S	A	S	T	K	G
P	S						
441	450	459	468	477	486		
GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC
AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG
GCC	CTG						
V	F	P	L	A	P	S	S
K	S	T	S	G	G	T	A
A	L						
495	504	513	522	531	540		
GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC
CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG
AAC	TCA						
G	C	L	V	K	D	Y	F
P	E	P	V	T	V	S	W
N	S						
549	558	567	576	585	594		
GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC
ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC
TCA	GGA						
G	A	L	T	S	G	V	H
T	F	P	A	V	L	Q	S
S	S	G					
603	612	621	630	639	648		
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG
ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC
ACC	CAG						
L	Y	S	L	S	S	V	V
T	V	P	S	S	S	L	G
T	Q						
657	666	675	684	693	702		

ACC	TAC	ATC	TGC	ATC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	ATC	GTG	GAC	AAG	AAA
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711			720			729			738			747			756		
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P
765			774			783			792			801			810		
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T
819			828			837			846			855			864		
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H
873			882			891			900			909			918		
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N
927			936			945			954			963			972		
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S
981			990			999			1008			1017			1026		
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K
1035			1044			1053			1062			1071			1080		
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K
1089			1098			1107			1116			1125			1134		
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L
1143			1152			1161			1170			1179			1188		
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D
1197			1206			1215			1224			1233			1242		
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T
1251			1260			1269			1278			1287			1296		
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V
1305			1314			1323			1332			1341			1350		
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC	TAC ACG CAG AAG AGC CTC TCC CTG TCG	TAC ACG CAG AAG AGC CTC TCC CTG TCG	TAC ACG CAG AAG AGC CTC TCC CTG TCG	TAC ACG CAG AAG AGC CTC TCC CTG TCG	TAC ACG CAG AAG AGC CTC TCC CTG TCG
A L H N	H Y T Q K S L S L S P K	H Y T Q K S L S L S P K	H Y T Q K S L S L S P K	H Y T Q K S L S L S P K	H Y T Q K S L S L S P K
1413	1422	1431	1440	1449	1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG	GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG	GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG	GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG	GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG	GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG
G G L K I A A F N I Q T F G E T K M	G G L K I A A F N I Q T F G E T K M	G G L K I A A F N I Q T F G E T K M	G G L K I A A F N I Q T F G E T K M	G G L K I A A F N I Q T F G E T K M	G G L K I A A F N I Q T F G E T K M
1467	1476	1485	1494	1503	1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC	TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC	TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC	TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC	TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC	TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC
S N A T L V S Y I V Q I L S R Y D I	S N A T L V S Y I V Q I L S R Y D I	S N A T L V S Y I V Q I L S R Y D I	S N A T L V S Y I V Q I L S R Y D I	S N A T L V S Y I V Q I L S R Y D I	S N A T L V S Y I V Q I L S R Y D I
1521	1530	1539	1548	1557	1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG	GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG	GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG	GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG	GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG	GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG
A L V Q E V R D S H L T A V G K L L	A L V Q E V R D S H L T A V G K L L	A L V Q E V R D S H L T A V G K L L	A L V Q E V R D S H L T A V G K L L	A L V Q E V R D S H L T A V G K L L	A L V Q E V R D S H L T A V G K L L
1575	1584	1593	1602	1611	1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA	GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA	GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA	GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA	GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA	GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA
D N L N Q D A P D T Y H Y V V S E P	D N L N Q D A P D T Y H Y V V S E P	D N L N Q D A P D T Y H Y V V S E P	D N L N Q D A P D T Y H Y V V S E P	D N L N Q D A P D T Y H Y V V S E P	D N L N Q D A P D T Y H Y V V S E P
1629	1638	1647	1656	1665	1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG	CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG	CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG	CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG	CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG	CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG
L G R N S Y K E R Y L F V Y R P D Q	L G R N S Y K E R Y L F V Y R P D Q	L G R N S Y K E R Y L F V Y R P D Q	L G R N S Y K E R Y L F V Y R P D Q	L G R N S Y K E R Y L F V Y R P D Q	L G R N S Y K E R Y L F V Y R P D Q
1683	1692	1701	1710	1719	1728
GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC	GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC	GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC	GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC	GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC	GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC
V S A V D S Y Y Y D D G C E P C G N	V S A V D S Y Y Y D D G C E P C G N	V S A V D S Y Y Y D D G C E P C G N	V S A V D S Y Y Y D D G C E P C G N	V S A V D S Y Y Y D D G C E P C G N	V S A V D S Y Y Y D D G C E P C G N
1737	1746	1755	1764	1773	1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG	GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG	GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG	GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG	GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG	GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG
D T F N R E P A I V R F F S R F T E	D T F N R E P A I V R F F S R F T E	D T F N R E P A I V R F F S R F T E	D T F N R E P A I V R F F S R F T E	D T F N R E P A I V R F F S R F T E	D T F N R E P A I V R F F S R F T E
1791	1800	1809	1818	1827	1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC	GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC	GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC	GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC	GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC	GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC
V R E F A I V P L H A A P G D A V A	V R E F A I V P L H A A P G D A V A	V R E F A I V P L H A A P G D A V A	V R E F A I V P L H A A P G D A V A	V R E F A I V P L H A A P G D A V A	V R E F A I V P L H A A P G D A V A
1845	1854	1863	1872	1881	1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG	GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG	GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG	GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG	GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG	GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG
E I D A L Y D V Y L D V Q E K W G L	E I D A L Y D V Y L D V Q E K W G L	E I D A L Y D V Y L D V Q E K W G L	E I D A L Y D V Y L D V Q E K W G L	E I D A L Y D V Y L D V Q E K W G L	E I D A L Y D V Y L D V Q E K W G L
1899	1908	1917	1926	1935	1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC	GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC	GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC	GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC	GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC	GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC
E D V M L M G D F N A G C S Y V R P	E D V M L M G D F N A G C S Y V R P	E D V M L M G D F N A G C S Y V R P	E D V M L M G D F N A G C S Y V R P	E D V M L M G D F N A G C S Y V R P	E D V M L M G D F N A G C S Y V R P
1953	1962	1971	1980	1989	1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC	TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC	TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC	TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC	TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC	TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC
S Q W S S I R L W T S P T F Q W L I	S Q W S S I R L W T S P T F Q W L I	S Q W S S I R L W T S P T F Q W L I	S Q W S S I R L W T S P T F Q W L I	S Q W S S I R L W T S P T F Q W L I	S Q W S S I R L W T S P T F Q W L I
2007	2016	2025	2034	2043	2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC	CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC	CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC	CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC	CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC	CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC
P D S A D T T A T P T H C A Y D R I	P D S A D T T A T P T H C A Y D R I	P D S A D T T A T P T H C A Y D R I	P D S A D T T A T P T H C A Y D R I	P D S A D T T A T P T H C A Y D R I	P D S A D T T A T P T H C A Y D R I

2061			2070			2079			2088			2097			2106		
GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT	CCC
-----																	
V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L	P
-----																	
2115			2124			2133			2142			2151			2160		
TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	AGT
-----																	
F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I	S
-----																	
2169			2178			2187											
GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'						
-----																	
D	H	Y	P	V	E	V	M	L	K	*							

## (A) pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 36  
 DEFINITION Clone 18.24.1 with residue 1392 T > C  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS83 and AS84  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 FEATURES Residue 1392 T > C silent S to S mutation  
 SITES Note  
 BASE COUNT 498 a 678 c 605 g 409 t  
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CCGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCAAC
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA CCGTCTTCCC CGTCTTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA

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FIGURE 9 (B)

1. The first group of people who are interested in the study of the history of the world are the historians. They are people who study the past and try to understand what happened and why it happened. They use a variety of sources, including books, documents, and artifacts, to reconstruct the past.

ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA				
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K				
-----																					
711				720				729				738				747				756	
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT				
-----																					
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P				
-----																					
765				774				783				792				801				810	
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC				
-----																					
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T				
-----																					
819				828				837				846				855				864	
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC				
-----																					
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H				
-----																					
873				882				891				900				909				918	
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT				
-----																					
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N				
-----																					
927				936				945				954				963				972	
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC				
-----																					
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S				
-----																					
981				990				999				1008				1017				1026	
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG				
-----																					
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K				
-----																					
1035				1044				1053				1062				1071				1080	
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA				
-----																					
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K				
-----																					
1089				1098				1107				1116				1125				1134	
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG				
-----																					
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L				
-----																					
1143				1152				1161				1170				1179				1188	
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC				
-----																					
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D				
-----																					
1197				1206				1215				1224				1233				1242	
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG				
-----																					
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T				
-----																					
1251				1260				1269				1278				1287				1296	
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG				
-----																					
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V				
-----																					
1305				1314				1323				1332				1341				1350	
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG				
-----																					
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E				

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC					
A L H N H Y T Q K S L S L S P <u>G S G</u>					
1413	1422	1431	1440	1449	1458
GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC					
<u>G</u> L K I A A F N I Q T F G E T K M S					
1467	1476	1485	1494	1503	1512
AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC					
N A T L V S Y I V Q I L S R Y D I A					
1521	1530	1539	1548	1557	1566
CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC					
L V Q E V R D S H L T A V G K L L D					
1575	1584	1593	1602	1611	1620
AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG					
N L N Q D A P D T Y H Y V V S E P L					
1629	1638	1647	1656	1665	1674
GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG					
G R N S Y K E R Y L F V Y R P D Q V					
1683	1692	1701	1710	1719	1728
TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC					
S A V D S Y Y Y D D G C E P C G N D					
1737	1746	1755	1764	1773	1782
ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC					
T F N R E P A I V R F F S R F T E V					
1791	1800	1809	1818	1827	1836
AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG					
R E F A I V P L H A A P G D A V A E					
1845	1854	1863	1872	1881	1890
ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG					
I D A L Y D V Y L D V Q E K W G L E					
1899	1908	1917	1926	1935	1944
GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC					
D V M L M G D F N A G C S Y V R P S					
1953	1962	1971	1980	1989	1998
CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC					
Q W S S I R L W T S P T F Q W L I P					
2007	2016	2025	2034	2043	2052
GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG					
D S A D T T A T P T H C A Y D R I V					

2061				2070				2079				2088				2097				2106			
GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT	CCC	TTT						
-----																							
V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L	P	F						
-----																							
2115				2124				2133				2142				2151				2160			
AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	AGT	GAC						
-----																							
N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I	S	D						
-----																							
2169				2178				2187															
CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'													
-----																							
H	Y	P	V	E	V	M	L	K	*														

## (A) pAS37

LOCUS PAS37.DNA 2226 bp 2196 bp 2196 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 37  
 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) plus NLS  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS79 and AS80  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 SITES Note  
 BASE COUNT 511 a 683 c 619 g 413 t  
 ORIGIN ?

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAActCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTAGTC
781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAAACA TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GTTCAGTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCTG TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCAGAGAG CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCCTCC CAGTGGTCAT CCATCCGCCT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCAGACAG GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAACCTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGCG GACCCAAAAA GAAGCGCAAG
2221 GTTTGA

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↳ NLS

FIGURE 10 (B)

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ACC	TAC	ATC	TGC	ATC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAC	GTG	GAC	AAG	AAA				
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K				
-----																					
711				720				729				738				747				756	
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT				
-----																					
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P				
-----																					
765				774				783				792				801				810	
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC				
-----																					
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T				
-----																					
819				828				837				846				855				864	
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC				
-----																					
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H				
-----																					
873				882				891				900				909				918	
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT				
-----																					
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N				
-----																					
927				936				945				954				963				972	
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC				
-----																					
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S				
-----																					
981				990				999				1008				1017				1026	
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG				
-----																					
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K				
-----																					
1035				1044				1053				1062				1071				1080	
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA				
-----																					
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K				
-----																					
1089				1098				1107				1116				1125				1134	
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG				
-----																					
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L				
-----																					
1143				1152				1161				1170				1179				1188	
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC				
-----																					
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D				
-----																					
1197				1206				1215				1224				1233				1242	
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG				
-----																					
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T				
-----																					
1251				1260				1269				1278				1287				1296	
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG				
-----																					
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V				
-----																					
1305				1314				1323				1332				1341				1350	
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG				
-----																					
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E				

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA GGG					
A L H N H Y T Q K S L S L S P G K <u>G</u>					
1413	1422	1431	1440	1449	1458
AGC GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
<u>S G G</u> L K I A A F N I Q T F G E T K					
1467	1476	1485	1494	1503	1512
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
M S N A T L V S Y I V Q I L S R Y D					
1521	1530	1539	1548	1557	1566
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
I A L V Q E V R D S H L T A V G K L					
1575	1584	1593	1602	1611	1620
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
L D N L N Q D A P D T Y H Y V V S E					
1629	1638	1647	1656	1665	1674
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
P L G R N S Y K E R Y L F V Y R P D					
1683	1692	1701	1710	1719	1728
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
Q V S A V D S Y Y Y D D G C E P C G					
1737	1746	1755	1764	1773	1782
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA					
N D T F N R E P A I V R F F S R F T					
1791	1800	1809	1818	1827	1836
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
E V R E F A I V P L H A A P G D A V					
1845	1854	1863	1872	1881	1890
GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC					
A E I D A L Y D V Y L D V Q E K W G					
1899	1908	1917	1926	1935	1944
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA					
L E D V M L M G D F N A G C S Y V R					
1953	1962	1971	1980	1989	1998
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG					
P S Q W S S I R L W T S P T F Q W L					
2007	2016	2025	2034	2043	2052
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG					
I P D S A D T T A T P T H C A Y D R					

2061	2070	2079	2088	2097	2106
ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT					
I V V A G M L L R G A V V P D S A L					
2115	2124	2133	2142	2151	2160
CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC					
P F N F Q A A Y G L S D Q L A Q A I					
2169	2178	2187	2196	2205	2214
AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG					
S D H Y P V E V M L K <u>G G G P K K K</u>					
2223					
CGC AAG GTT TGA 3'					
<u>R K V</u> *					

## (A) pAS38

LOCUS PAS38.DNA 2223 bp 2193 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 38  
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS81 and AS82  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)  
 SITES Note  
 BASE COUNT 510 a 683 c 618 g 412 t  
 ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG  
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC  
 121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA  
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT  
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG  
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC  
 361 TTTGCCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC  
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACACGCG  
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA  
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC  
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC  
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT  
 721 GACAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC  
 781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCGGACCCC TGAGGTCACA  
 841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC  
 901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC  
 961 CGTGTGGTCA GCGTCCCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG  
 1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA  
 1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCAT CCCGGGATGA GCTGACCAAG  
 1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG  
 1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCTCCCGT GCTGGACTCC  
 1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG  
 1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC  
 1381 CTCTCCCTGT CTCCGAAGGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA  
 1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC  
 1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG  
 1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA  
 1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT  
 1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC  
 1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTACAG AGGTCAGGGA GTTTGCCATT  
 1801 GTTCCCTGTC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC  
 1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTGATGGG CGACTTCAAT  
 1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC  
 1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC  
 2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC GCACTCGGCT  
 2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT  
 2161 GACCACTATC CAGTGGAGGT GATGCTGAAG GGGGGCGGAC CCAAAAGAA GCGCAAGGTT  
 2221 TGA

//

L3MLS

File : PAS38.DNA  
 Range : 1 - 2223 Mode : Normal  
 Codon Table : Universal

FIGURE 11 (B)

	9				18				27				36				45				54			
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC						
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H						
	63				72				81				90				99				108			
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA						
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S						
	117				126				135				144				153				162			
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG						
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E						
	171				180				189				198				207				216			
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT						
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P						
	225				234				243				252				261				270			
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT						
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T						
	279				288				297				306				315				324			
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG						
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E						
	333				342				351				360				369				378			
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC						
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y						
	387				396				405				414				423				432			
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG						
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S						
	441				450				459				468				477				486			
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG						
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L						
	495				504				513				522				531				540			
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA						
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S						
	549				558				567				576				585				594			
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA						
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G						
	603				612				621				630				639				648			
	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG						
	L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q						
	657				666				675				684				693				702			

ACC	TAC	ATC	TGC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	ATG	GAC	AAG	AAA								
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D								
-----																							
711				720				729				738				747				756			
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT						
-----																							
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P						
-----																							
765				774				783				792				801				810			
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG	GAC	ACC						
-----																							
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D	T						
-----																							
819				828				837				846				855				864			
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC						
-----																							
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H						
-----																							
873				882				891				900				909				918			
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT						
-----																							
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V	H	N						
-----																							
927				936				945				954				963				972			
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC						
-----																							
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S						
-----																							
981				990				999				1008				1017				1026			
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG						
-----																							
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K	C	K						
-----																							
1035				1044				1053				1062				1071				1080			
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA						
-----																							
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K						
-----																							
1089				1098				1107				1116				1125				1134			
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG						
-----																							
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L						
-----																							
1143				1152				1161				1170				1179				1188			
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC	AGC	GAC						
-----																							
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D						
-----																							
1197				1206				1215				1224				1233				1242			
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG	ACC	ACG						
-----																							
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T						
-----																							
1251				1260				1269				1278				1287				1296			
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG						
-----																							
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V						
-----																							
1305				1314				1323				1332				1341				1350			
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG						
-----																							
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M	H	E						

1359	1368	1377	1386	1395	1404
GCT CTG CAC AAC CAC TAC	ACG CAG AAG AGC CTC TCC CTG TCT CCG AAG GGG AGC				
A L H N H Y T Q K S L S L S P K	<u>G S</u>				
1413	1422	1431	1440	1449	1458
GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG					
<u>G G</u> L K I A A F N I Q T F G E T K M					
1467	1476	1485	1494	1503	1512
TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC					
S N A T L V S Y I V Q I L S R Y D I					
1521	1530	1539	1548	1557	1566
GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG					
A L V Q E V R D S H L T A V G K L L					
1575	1584	1593	1602	1611	1620
GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA					
D N L N Q D A P D T Y H Y V V S E P					
1629	1638	1647	1656	1665	1674
CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG					
L G R N S Y K E R Y L F V Y R P D Q					
1683	1692	1701	1710	1719	1728
GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC					
V S A V D S Y Y Y D D G C E P C G N					
1737	1746	1755	1764	1773	1782
GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG					
D T F N R E P A I V R F F S R F T E					
1791	1800	1809	1818	1827	1836
GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC					
V R E F A I V P L H A A P G D A V A					
1845	1854	1863	1872	1881	1890
GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG					
E I D A L Y D V Y L D V Q E K W G L					
1899	1908	1917	1926	1935	1944
GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC					
E D V M L M G D F N A G C S Y V R P					
1953	1962	1971	1980	1989	1998
TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC					
S Q W S S I R L W T S P T F Q W L I					
2007	2016	2025	2034	2043	2052
CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC					
P D S A D T T A T P T H C A Y D R I					

2061				2070				2079				2088				2097				2106			
GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT	CCC						
-----																							
V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L	P						
-----																							
2115				2124				2133				2142				2151				2160			
TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC	AGT						
-----																							
F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I	S						
-----																							
2169				2178				2187				2196				2205				2214			
GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	GGG	GGC	GGA	CCC	AAA	AAG	AAG	CGC						
-----																							
D	H	Y	P	V	E	V	M	L	K	<u>G</u>	<u>G</u>	<u>G</u>	<u>P</u>	<u>K</u>	<u>K</u>	<u>K</u>	<u>R</u>						

2223  
AAG GTT TGA 3'

-----  
K V \*

FIGURE

## (4) pAS39

LOCUS PAS39.DNA 2220 bp 2190 bp DNA 14-AUG-1998  
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 39  
 DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS  
 REFERENCE  
 AUTHORS VERHOEYEN ET AL  
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc  
 JOURNAL IMMUNOL. (1993):78, 364-370  
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)  
 COMMENT The fusion was made using overlapping oligos AS83 and AS84  
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)  
 FEATURES Residue 963 is G > T leading to silent mutation in all clones  
 FEATURES Residue 1392 T > C silent S to S mutation  
 SITES Note  
 BASE COUNT 508 a 684 c 617 g 411 t  
 ORIGIN ?

```

1  ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61  GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTGAGTC
781 TTCCTCTTCC CCCCCAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTACA
841 TGGCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

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File : PAS39.DNA  
 Range : 1 - 2220 Mode : Normal  
 Codon Table : Universal

FIGURE 12(B)

5'	9	18	27	36	45	54
ATG	GGA	TGG	AGC	TGT	ATC	ATC
ATC	CTC	TTC	TTG	GTA	GCA	ACA
GCT	ACA	GCT	ACA	GGT	GTC	CAC
M	G	W	S	C	I	I
L	F	L	V	A	T	A
T	G	V	H			
63	72	81	90	99	108	
TCC	CAG	GTG	CAG	CTG	GTG	CAG
TCT	GGG	GCA	GAG	GTG	AAA	AAG
CCT	GGG	GCC	TCA			
S	Q	V	Q	L	V	Q
S	G	A	E	V	K	K
P	G	A	S			
117	126	135	144	153	162	
GTG	AAG	GTG	TCC	TGC	AAG	GCT
TCT	GGC	TAC	ACC	TTC	AGT	GCC
TAC	TGG	ATA	GAG			
V	K	V	S	C	K	A
S	G	Y	T	F	S	A
Y	W	I	E			
171	180	189	198	207	216	
TGG	GTG	CGC	CAG	GCT	CCA	GGA
AAG	GGC	CTC	GAG	TGG	GTC	GGA
GAG	ATT	TTA	CCT			
W	V	R	Q	A	P	G
K	G	L	E	W	V	G
E	I	L	P			
225	234	243	252	261	270	
GGA	AGT	AAT	AAT	TCT	AGA	TAC
AAT	GAG	AAG	TTC	AAG	GGC	CGA
GTG	ACA	GTC	ACT			
G	S	N	N	S	R	Y
N	E	K	F	K	G	R
V	T	V	T			
279	288	297	306	315	324	
AGA	GAC	ACA	TCC	ACA	AAC	ACA
GCC	TAC	ATG	GAG	CTC	AGC	AGC
CTG	AGG	TCT	GAG			
R	D	T	S	T	N	T
A	Y	M	E	L	S	S
L	R	S	E			
333	342	351	360	369	378	
GAC	ACA	GCC	GTC	TAT	TAC	TGT
GCA	AGA	TCC	TAC	GAC	TTT	GCC
TGG	TTT	GCC	TGG	TTT	GCT	TAC
D	T	A	V	Y	Y	C
A	R	S	Y	D	F	A
W	F	A	W	F	A	Y
387	396	405	414	423	432	
TGG	GGC	CAA	GGG	ACT	CTG	GTC
ACA	GTC	TCC	TCA	GCC	TCC	ACC
AAG	GGC	CCA	TCG			
W	G	Q	G	T	L	V
T	V	S	S	A	S	T
K	G	P	S			
441	450	459	468	477	486	
GTC	TTC	CCC	CTG	GCA	CCC	TCC
TCC	TCC	AAG	AGC	ACC	TCT	GGG
GGC	ACA	GCG	GCC	CTG		
V	F	P	L	A	P	S
S	S	K	S	T	S	G
G	G	T	A	A	L	
495	504	513	522	531	540	
GGC	TGC	CTG	GTC	AAG	GAC	TAC
TTC	CCC	GAA	CCG	GTG	ACG	GTG
TCG	TGG	AAC	TCA			
G	C	L	V	K	D	Y
F	P	E	P	V	T	V
S	W	N	S			
549	558	567	576	585	594	
GGC	GCC	CTG	ACC	AGC	GGC	GTG
CAC	ACC	TTC	CCG	GCT	GTC	CTA
CAG	TCC	TCA	GGA			
G	A	L	T	S	G	V
H	T	F	P	A	V	L
Q	S	S	G			
603	612	621	630	639	648	
CTC	TAC	TCC	CTC	AGC	AGC	GTG
GTG	ACC	GTG	CCC	TCC	AGC	AGC
TTG	GGC	ACC	CAG			
L	Y	S	L	S	S	V
V	T	V	P	S	S	S
L	G	T	Q			
657	666	675	684	693	702	

ACC	TAC	ATC	TG	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	GTG	GAC	AAG	AAA
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D
711	720	729	738	747	756										
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P
765	774	783	792	801	810										
GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC	AAG
E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K
819	828	837	846	855	864										
CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG	GTG	GAC	GTG
L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V
873	882	891	900	909	918										
GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG
E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V
927	936	945	954	963	972										
GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG
A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V
981	990	999	1008	1017	1026										
GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG
V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K
1035	1044	1053	1062	1071	1080										
GTC	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA
V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K
1089	1098	1107	1116	1125	1134										
GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT
G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D
1143	1152	1161	1170	1179	1188										
ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAT	CCC
T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P
1197	1206	1215	1224	1233	1242										
ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	GAG	AAC	AAC	TAC	AAG
I	A	V	E	W	E	S	N	G	Q	P	E	N	N	Y	K
1251	1260	1269	1278	1287	1296										
CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AAG	CTC
P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L
1305	1314	1323	1332	1341	1350										
GAC	AAG	AGC	AGG	TGG	CAG	CAG	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG
D	K	S	R	W	Q	Q	G	N	V	F	S	C	S	V	M

1359	68	1377	1386	1404
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A L H N H Y T Q K S L S L S P	<u>G S G</u>			
1413	1422	1431	1440	1449
GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC				
<u>G</u> L K I A A F N I Q T F G E T K M S				
1467	1476	1485	1494	1503
AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC				
N A T L V S Y I V Q I L S R Y D I A				
1521	1530	1539	1548	1557
CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC				
L V Q E V R D S H L T A V G K L L D				
1575	1584	1593	1602	1611
AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG				
N L N Q D A P D T Y H Y V V S E P L				
1629	1638	1647	1656	1665
GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG				
G R N S Y K E R Y L F V Y R P D Q V				
1683	1692	1701	1710	1719
TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC				
S A V D S Y Y Y D D G C E P C G N D				
1737	1746	1755	1764	1773
ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC				
T F N R E P A I V R F F S R F T E V				
1791	1800	1809	1818	1827
AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG				
R E F A I V P L H A A P G D A V A E				
1845	1854	1863	1872	1881
ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG				
I D A L Y D V Y L D V Q E K W G L E				
1899	1908	1917	1926	1935
GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC				
D V M L M G D F N A G C S Y V R P S				
1953	1962	1971	1980	1989
CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC				
Q W S S I R L W T S P T F Q W L I P				
2007	2016	2025	2034	2043
GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG				
D S A D T T A T P T H C A Y D R I V				

2061	2070	2079	2088	2097	2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT					
V A G M L L R G A V V P D S A L P F					
2115	2124	2133	2142	2151	2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC					
N F Q A A Y G L S D Q L A Q A I S D					
2169	2178	2187	2196	2205	2214
CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC AAG					
H Y P V E V M L K G <u>G G P K K K R K</u>					

GTT TGA 3'

V \*

(A) pAS101

LOCUS PAS101.DNA 1548 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 343 a 467 c 430 g 308 t  
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181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTA
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601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCTC ACACATGCCC ACCGTGCCCC GCACCTGAAG GCGGGCTGAA GATCGCAGCC
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841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
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1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGTCCG AGGGGCCGTT
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# Figure 13 (B)

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ACCESSION  -
KEYWORDS   -
SOURCE     -
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    181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
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    361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
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    481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAC TCA
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    601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
    661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
    721 GACAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
    781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
    841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
    901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
    961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
   1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
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   1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCGGGGGG ACGCAGTAGC CGAGATCGAC
   1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
   1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
   1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
   1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
   1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
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LOCUS FDDNASE101 1557 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
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 BASE COUNT 344 A 471 C 433 G 309 T 0 OTHER  
 ORIGIN -

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121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCAGG GACGGTGTCTG
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901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
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1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC
1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA
1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC
1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
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1501 GACCAACTGG CCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA

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File : PAS101.DNA  
 Range : 1 - 548 Mode : Normal  
 Codon Table : Universal

PLUKE B(D)

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	63	72	81	90	99	108												
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	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
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	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	225	234	243	252	261	270												
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	279	288	297	306	315	324												
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	387	396	405	414	423	432												
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	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	441	450	459	468	477	486												
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
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	495	504	513	522	531	540												
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	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	549	558	567	576	585	594												
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

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L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC	GTG AAT CAC AAG CCC	AGC AAC ACC AAG GTG GAC AAG AAA			
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711	720	729	738	747	756
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M S N A T L V S Y I V Q I L S R Y D					
873	882	891	900	909	918
ATC GCC CTG GTC CAG	GAG GTC AGA GAC	AGC CAC CTG ACT GCC	GTG GGG AAG CTG		
I A L V Q E V R D S H L T A V G K L					
927	936	945	954	963	972
CTG GAC AAC CTC AAT	CAG GAC GCA CCA	GAC ACC TAT CAC TAC	GTG GTC AGT GAG		
L D N L N Q D A P D T Y H Y V V S E					
981	990	999	1008	1017	1026
CCA CTG GGA CGG AAC	AGC TAT AAG GAG	CGC TAC CTG TTC	GTG TAC AGG CCT GAC		
P L G R N S Y K E R Y L F V Y R P D					
1035	1044	1053	1062	1071	1080
CAG GTG TCT GCG GTG	GAC AGC TAC TAC	TAC GAT GAT GGC	TGC GAG CCC TGC GGG		
Q V S A V D S Y Y Y D D G C E P C G					
1089	1098	1107	1116	1125	1134
AAC GAC ACC TTC AAC	CGA GAG CCA GCC	ATT GTC AGG TTC	TTC TCC CGG TTC ACA		
N D T F N R E P A I V R F F S R F T					
1143	1152	1161	1170	1179	1188
GAG GTC AGG GAG TTT	GCC ATT GTT CCC	CTG CAT GCG GCC	CCG GGG GAC GCA GTA		
E V R E F A I V P L H A A P G D A V					
1197	1206	1215	1224	1233	1242

GCC	GAG	ATC	GAC	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	GAG	AAA	TGG	GGC		
A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G
-----																	
1251				1260			1269			1278			1287		1296		
TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA
L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R
-----																	
1305				1314			1323			1332			1341		1350		
CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG
P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L
-----																	
1359				1368			1377			1386			1395		1404		
ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG
I	P	D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R
-----																	
1413				1422			1431			1440			1449		1458		
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L
-----																	
1467				1476			1485			1494			1503		1512		
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I
-----																	
1521				1530			1539			1548							
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'					
S	D	H	Y	P	V	E	V	M	L	K	*						

# FIGURE 1 (A) pAS102

LOCUS PAS102.DNA 1566 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna) (see Figure 2)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 345 a 469 c 440 g 312 t  
 ORIGIN

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCTG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGATCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA
  
```

//

LOCUS FDDNASE102 1566 BP SS-DNA SYN 23-MAR-2001  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -  
 BASE COUNT 345 A 468 C 440 G 313 T 0 OTHER  
 ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG  
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC  
 121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA  
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT  
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG  
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC  
 361 TTTGCTGGT TTTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC  
 421 AAGGGCCCCT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG  
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTA  
 541 GGCAGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC  
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC  
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT  
 721 GACAAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC  
 781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC  
 841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG  
 901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA  
 961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC  
 1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT  
 1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAG CAGCCATTGT CAGGTTCTTC  
 1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC  
 1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC  
 1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCTCC  
 1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCACAGC  
 1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG  
 1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT  
 1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG  
 1561 AAGTGA

Figure 14 (c)

LOCUS FDDNASE302 1575 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

pAS302

FEATURES Location/Qualifiers  
 frag 10..1575  
 /note="1 to 1566 of FdDNase102correct"

BASE COUNT 346 A 474 C 442 G 313 T 0 OTHER

ORIGIN -  
 1 CCCCCAACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC  
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG  
 121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC  
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT  
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA  
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA  
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA  
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG  
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCAGT GACGGTGTGCG  
 541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA  
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC  
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC  
 721 AAATCTTG TG ACAAACCTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG  
 781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG  
 841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG  
 901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT  
 961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT  
 1021 AAGGAGCGCT ACCTGTTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC  
 1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC  
 1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCTT GCATGCGGCC  
 1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG  
 1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG  
 1321 AGACCTTCCC AGTGGTCATC CATCCGCTTG TGGACAAGCC CCACCTTCCA GTGGCTGATC  
 1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT  
 1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG  
 1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG  
 1561 GTGATGCTGA AGTGA

File : PAS102.DNA  
 Range : 1 - 1566 Mode : Normal  
 Codon Table : Universal

FIGURE 14 (D)

		9			18				27			36			45			54
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
			63			72			81			90			99			108
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
			117			126			135			144			153			162
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
			171			180			189			198			207			216
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
			225			234			243			252			261			270
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
			279			288			297			306			315			324
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
			333			342			351			360			369			378
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
			387			396			405			414			423			432
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
			441			450			459			468			477			486
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
			495			504			513			522			531			540
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
			549			558			567			576			585			594
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

603			612			621			630			639			648		
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657			666			675			684			693			702		
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711			720			729			738			747			756		
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	TGT	GTG	GAG	TGC	CCA	CCG
V	E	P	K	S	C	D	K	T	H	T	C	C	V	E	C	P	P
765			774			783			792			801			810		
TGC	CCA	GCA	CCT	GAA	GGG	AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG
C	P	A	P	E	G	S	G	G	L	K	I	A	A	F	N	I	Q
819			828			837			846			855			864		
ACA	TTT	GGG	GAG	ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG
T	F	G	E	T	K	M	S	N	A	T	L	V	S	Y	I	V	Q
873			882			891			900			909			918		
ATC	CTG	AGC	CGC	TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG
I	L	S	R	Y	D	I	A	L	V	Q	E	V	R	D	S	H	L
927			936			945			954			963			972		
ACT	GCC	GTG	GGG	AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT
T	A	V	G	K	L	L	D	N	L	N	Q	D	A	P	D	T	Y
981			990			999			1008			1017			1026		
CAC	TAC	GTG	GTC	AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG
H	Y	V	V	S	E	P	L	G	R	N	S	Y	K	E	R	Y	L
1035			1044			1053			1062			1071			1080		
TTC	GTG	TAC	AGG	CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT
F	V	Y	R	P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D
1089			1098			1107			1116			1125			1134		
GGC	TGC	GAG	CCC	TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG
G	C	E	P	C	G	N	D	T	F	N	R	E	P	A	I	V	R
1143			1152			1161			1170			1179			1188		
TTC	TTC	TCC	CGG	TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG
F	F	S	R	F	T	E	V	R	E	F	A	I	V	P	L	H	A
1197			1206			1215			1224			1233			1242		

GCC	CCG	GGG	GAC	ATA	GTA	GCC	GAG	ATC	GAC	GCT	CTC	TAT	GTG	TAC	CTG	GAT	
A	P	G	D	A	V	A	E	I	D	A	L	Y	D	V	Y	L	D
-----																	
1251				1260			1269			1278			1287			1296	
GTG	CAA	GAG	AAA	TGG	GGC	TTG	GAG	GAC	GTG	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG
V	Q	E	K	W	G	L	E	D	V	M	L	M	G	D	F	N	A
-----																	
1305				1314			1323			1332			1341			1350	
GGC	TGC	AGC	TAT	GTG	AGA	CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC
G	C	S	Y	V	R	P	S	Q	W	S	S	I	R	L	W	T	S
-----																	
1359				1368			1377			1386			1395			1404	
CCC	ACC	TTC	CAG	TGG	CTG	ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG
P	T	F	Q	W	L	I	P	D	S	A	D	T	T	A	T	P	T
-----																	
1413				1422			1431			1440			1449			1458	
CAC	TGT	GCC	TAT	GAC	AGG	ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT
H	C	A	Y	D	R	I	V	V	A	G	M	L	L	R	G	A	V
-----																	
1467				1476			1485			1494			1503			1512	
GTT	CCC	GAC	TCG	GCT	CTT	CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC
V	P	D	S	A	L	P	F	N	F	Q	A	A	Y	G	L	S	D
-----																	
1521				1530			1539			1548			1557			1566	
CAA	CTG	GCC	CAA	GCC	ATC	AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA 3'
Q	L	A	Q	A	I	S	D	H	Y	P	V	E	V	M	L	K	*

FIGURE 15

(A) pAS103

LOCUS PAS103.DNA 1560 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 344 a 468 c 436 g 312 t  
 ORIGIN

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGAAGTCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
  
```

//

# Figure 1S (B)

LOCUS FDDNASE103 1560 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

Location/Qualifiers

frag join(1..>720,<793..1560)

/note="1 to 1560 of PAS103.dna [Split]"

frag 721..792

/note="1 to 72 of 103/107linker"

frag join(721..>771,<772..792)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 344 A 467 C 436 G 313 T 0 OTHER

ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC

121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA

181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT

241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG

301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC

361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC

421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG

481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA

541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC

601 TCCCTCAGCA GCGTGCTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC

661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT

721 GACAAAACCTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG

781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC

841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA

901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC

961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG

1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC

1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG

1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA

1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG

1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG

1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC

1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC

1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG

1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

LOCUS FDDNASE103 1569 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
 frag 10..1569  
 /note="1 to 1560 of FdDNase103correct"  
 frag join(10..>729,<802..1569)  
 /note="1 to 1560 of PAS103.dna [Split]"  
 frag 730..801  
 /note="1 to 72 of 103/107linker"  
 frag join(730..>780,<781..801)  
 /note="1 to 78 of 102linker [Split]"

BASE COUNT 345 A 473 C 438 G 313 T 0 OTHER  
 ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC  
 61 CACTCCCAGG TGCAGTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG  
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC  
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT  
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA  
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA  
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA  
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG  
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG  
 541 TGGAACCTAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA  
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC  
 661 TACATCTGCA ACGTGAATCA CAAGCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC  
 721 AAATCTTGTG ACAAAACTCA CACATGCTGT GTGAGGTGTC CACCGTGTCC AGCACCAGAG  
 781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT  
 841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG  
 901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC  
 961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG  
 1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT  
 1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTGAGTTT  
 1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTT CCCTGCATGC GGCCCCGGGG  
 1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG  
 1261 GGCTTGAGAG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC  
 1321 TCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC  
 1381 AGCGCTGACA CCACAGCTAC ACCCAGGCAC TGTGCCTATG ACAGGATCGT GGTGTCAGGG  
 1441 ATGCTGCTCC GAGGGGCCGT TGTTCCTGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC  
 1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG  
 1561 CTGAAGTGA

FIGURE 15 (D)

[illegible]

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT					
C P A P E G G L K I A A F N I Q T F					
819	828	837	846	855	864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG					
G E T K M S N A T L V S Y I V Q I L					
873	882	891	900	909	918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC					
S R Y D I A L V Q E V R D S H L T A					
927	936	945	954	963	972
GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC					
V G K L L D N L N Q D A P D T Y H Y					
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG					
V V S E P L G R N S Y K E R Y L F V					
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC					
Y R P D Q V S A V D S Y Y Y D D G C					
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC					
E P C G N D T F N R E P A I V R F F					
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG					
S R F T E V R E F A I V P L H A A P					
1197	1206	1215	1224	1233	1242

GGG	GAC	GCA	GTA	ATC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	CTG	GAT	GTC	CAA			
G	D	A	V	A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q		
1251				1260				1269				1278				1287		1296	
GAG	AAA	TGG	GGC	TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC		
E	K	W	G	L	E	D	V	M	L	M	G	D	F	N	A	G	C		
1305				1314				1323				1332				1341		1350	
AGC	TAT	GTG	AGA	CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC		
S	Y	V	R	P	S	Q	W	S	S	I	R	L	W	T	S	P	T		
1359				1368				1377				1386				1395		1404	
TTC	CAG	TGG	CTG	ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT		
F	Q	W	L	I	P	D	S	A	D	T	T	A	T	P	T	H	C		
1413				1422				1431				1440				1449		1458	
GCC	TAT	GAC	AGG	ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC		
A	Y	D	R	I	V	V	A	G	M	L	L	R	G	A	V	V	P		
1467				1476				1485				1494				1503		1512	
GAC	TCG	GCT	CTT	CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG		
D	S	A	L	P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L		
1521				1530				1539				1548				1557			
GCC	CAA	GCC	ATC	AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'			
A	Q	A	I	S	D	H	Y	P	V	E	V	M	L	K	*				

FIGURE

# (A) pAS104

LOCUS PAS104.DNA 1560 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)  
 Position 924 G to A by ggg to gag  
 Linker GR instead of GG (position 777)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 346 a 468 c 434 g 312 t  
 ORIGIN

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTA
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601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGAAGTCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
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1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

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//

LOCUS FDDNASE104 1560 BP SS-DNA SYN 25-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
 frag join(1..>720,<793..1560)  
 /note="1 to 1560 of PAS104.dna [Split]"  
 frag 721..792  
 /note="1 to 72 of 104linker"  
 frag join(721..>774,<776..792)  
 /note="1 to 72 of 103linker [Split]"  
 frag join(721..>771,<772..>774,<776..792)  
 /note="1 to 78 of 102linker [Split]"

BASE COUNT 346 A 467 C 434 G 313 T 0 OTHER

ORIGIN -  
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG  
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC  
 121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA  
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT  
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG  
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC  
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC  
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG  
 481 GCCCTGGGCT GCCTGGTCAA GGACTIONC CCCGAACCGG TGACGGTGTG GTGGAATCA  
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC  
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC  
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT  
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCAGGCTG  
 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCTC  
 841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA  
 901 GACAGCCACC TGACTGCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC  
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG  
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 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCAGTGG  
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC  
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC  
 1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG  
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

FIGURE 16(C)

		9			18				27			36			45			54
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
			63			72			81			90			99			108
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
			117			126			135			144			153			162
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
			171			180			189			198			207			216
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
			225			234			243			252			261			270
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
			279			288			297			306			315			324
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
			333			342			351			360			369			378
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
			387			396			405			414			423			432
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
			441			450			459			468			477			486
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
			495			504			513			522			531			540
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
			549			558			567			576			585			594
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

603	612	621	630	639	648
CTC TAC TCC CTC AGC	AGC GTG GTG ACC GTG CCC	TCC AGC AGC TTG GGC ACC CAG			
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGC AGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT					
C P A P E G R L K I A A F N I Q T F					
819	828	837	846	855	864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG					
G E T K M S N A T L V S Y I V Q I L					
873	882	891	900	909	918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC					
S R Y D I A L V Q E V R D S H L T A					
927	936	945	954	963	972
GTG GAG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC					
V E K L L D N L N Q D A P D T Y H Y					
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG					
V V S E P L G R N S Y K E R Y L F V					
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC					
Y R P D Q V S A V D S Y Y Y D D G C					
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC					
E P C G N D T F N R E P A I V R F F					
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG					
S R F T E V R E F A I V P L H A A P					
1197	1206	1215	1224	1233	1242

GGG	GAC	GCA	GTA	GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	D	A	V	A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q

1251	1260	1269	1278	1287	1296
GAG AAA TGG GGC TTG	GAG GAC GTC ATG TTG	ATG GGC GAC TTC AAT	GCG GGC TGC		
---	---	---	---	---	---
E K W G L E D V M L M G D F N A G C					

1305	1314	1323	1332	1341	1350
AGC TAT GTG AGA CCC TCC	CAG TGG TCA TCC	ATC CGC CTG TGG	ACA AGC CCC	ACC	
---	---	---	---	---	---
S Y V R P S Q W S S I R L W T S P T					

1359	1368	1377	1386	1395	1404
TTC CAG TGG CTG ATC CCC	GAC AGC GCT GAC ACC	ACA GCT ACA CCC	ACG CAC TGT		
---	---	---	---	---	---
F Q W L I P D S A D T T A T P T H C					

1413	1422	1431	1440	1449	1458
GCC TAT GAC AGG ATC GTG	GTT GCA GGG ATG CTG	CTC CGA GGG GCC	GTT GTT CCC		
---	---	---	---	---	---
A Y D R I V V A G M L L R G A V V P					

1467	1476	1485	1494	1503	1512
GAC TCG GCT CTT CCC TTT	AAC TTC CAG GCT GCC	TAT GGC CTG AGT	GAC CAA CTG		
---	---	---	---	---	---
D S A L P F N F Q A A Y G L S D Q L					

1521	1530	1539	1548	1557
GCC CAA GCC ATC AGT GAC	CAC TAT CCA GTG GAG	GTG ATG CTG AAG	TGA 3'	
---	---	---	---	---
A Q A I S D H Y P V E V M L K *				

(A) pAS105

LOCUS PAS105.DNA 1578 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS105)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 353 a 473 c 442 g 310 t  
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAC TCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCCTC AGGACTCTAC
601 TCCCTCAGCA CGGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCTCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGAGGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
1561 AAGAAGCGCA AGGTTTGA

```

//

↳ NLS

# Figure 17(B)

LOCUS FDDNASE105 1578 BP SS-DNA SYN 25-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -  
 FEATURES  
     frag join(1..>720,<781..1578)  
           /note="1 to 1578 of PAS105.dna [Split]"  
     frag 721..780  
           /note="1 to 60 of 101/105linker"  
     frag join(721..>735,<736..>759,<760..>780)  
           /note="1 to 80 of 102linker [Split]"  
 BASE COUNT 353 A 471 C 443 G 311 T 0 OTHER  
 ORIGIN -

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAATCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTCT AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGAGGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
1561 AAGAAGCGCA AGGTTTGA
  
```

Figure 17c

LOCUS FDDNASE105 1587 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -  
 FEATURES  
     Location/Qualifiers  
     frag 10..1587  
         /note="1 to 1578 of FdDNase105correct"  
     frag join(10..>729,<790..1587)  
         /note="1 to 1578 of PAS105.dna [Split]"  
     frag 730..789  
         /note="1 to 60 of 101/105linker"  
     frag join(730..>744,<745..>768,<769..>789)  
         /note="1 to 80 of 102linker [Split]"  
 BASE COUNT 354 A 477 C 445 G 311 T 0 OTHER  
 ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC  
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG  
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC  
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT  
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA  
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA  
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA  
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG  
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG  
 541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA  
 601 GGA CTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC  
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC  
 721 AAATCTTGTG AAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG  
 781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC  
 841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC  
 901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACTCA ATCAGGACGC ACCAGACACC  
 961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC  
 1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG  
 1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTT  
 1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCAGGGGA CGCAGTAGCC  
 1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC  
 1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA  
 1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC  
 1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA  
 1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTAACTTCC AGGCTGCCTA TGGCCTGAGT  
 1501 GACCAACTGG CCCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGGC  
 1561 GGACCCAAAA AGAAGCGCAA GGTTTGA

File : PAS105.DNA  
 Range : 1 1578 Mode : Normal  
 Codon Table : Universal

FIGURE 17 (D)

	9				18				27				36				45				54			
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC						
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H						
	63				72				81				90				99				108			
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA						
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S						
	117				126				135				144				153				162			
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG						
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E						
	171				180				189				198				207				216			
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT						
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P						
	225				234				243				252				261				270			
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT						
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T						
	279				288				297				306				315				324			
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG						
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E						
	333				342				351				360				369				378			
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC						
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y						
	387				396				405				414				423				432			
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG						
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S						
	441				450				459				468				477				486			
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG						
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L						
	495				504				513				522				531				540			
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA						
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S						
	549				558				567				576				585				594			
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA						
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G						

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT					
V E P K S C D K T H T C P P C P A P					
765	774	783	792	801	810
GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG					
E G G L K I A A F N I Q T F G E T K					
819	828	837	846	855	864
ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC					
M S N A T L V S Y I V Q I L S R Y D					
873	882	891	900	909	918
ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG					
I A L V Q E V R D S H L T A V G K L					
927	936	945	954	963	972
CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG					
L D N L N Q D A P D T Y H Y V V S E					
981	990	999	1008	1017	1026
CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC					
P L G R N S Y K E R Y L F V Y R P D					
1035	1044	1053	1062	1071	1080
CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG					
Q V S A V D S Y Y Y D D G C E P C G					
1089	1098	1107	1116	1125	1134
AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA					
N D T F N R E P A I V R F F S R F T					
1143	1152	1161	1170	1179	1188
GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA					
E V R E F A I V P L H A A P G D A V					
1197	1206	1215	1224	1233	1242

GCC GAG ATC GAT TCT CTC TAT GAC GTC TAC CTG GAT GTC GAG AAA TGG GGC  
 -----  
 A E I D A L Y D V Y L D V Q E K W G

1251 1260 1269 1278 1287 1296  
 TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA  
 -----  
 L E D V M L M G D F N A G C S Y V R

1305 1314 1323 1332 1341 1350  
 CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG  
 -----  
 P S Q W S S I R L W T S P T F Q W L

1359 1368 1377 1386 1395 1404  
 ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG  
 -----  
 I P D S A D T T A T P T H C A Y D R

1413 1422 1431 1440 1449 1458  
 ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT  
 -----  
 I V V A G M L L R G A V V P D S A L

1467 1476 1485 1494 1503 1512  
 CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC  
 -----  
 P F N F Q A A Y G L S D Q L A Q A I

1521 1530 1539 1548 1557 1566  
 AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG  
 -----  
 S D H Y P V E V M L K G G G P K K K

1575  
 CGC AAG GTT TGA 3'  
 -----  
 R K V \*

FIGURE 1

# (A) pAS106

LOCUS PAS106.DNA 1596 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS106)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 355 a 475 c 452 g 314 t  
 ORIGIN

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCCTC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAAGTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

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//

↳ NLS

LOCUS FDDNASE106 1596 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

frag join(1..>720,<799..1596)  
/note="1 to 1596 of PAS106.dna [Split]"

frag 721..798  
/note="1 to 78 of 102/106linker"

BASE COUNT 355 A 474 C 452 G 315 T 0 OTHER

ORIGIN -

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAActCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAG CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

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LOCUS FDDNASE106 1605 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

frag 10..1605

frag join(10..>729,<808..1605)

frag 730..807

Location/Qualifiers

/note="1 to 1596 of FdDNase106correct"

/note="1 to 1596 of PAS106.dna [Split]"

/note="1 to 78 of 102/106linker"

BASE COUNT 356 A 480 C 454 G 315 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC

61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG

121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC

181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT

241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA

301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA

361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA

421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG

481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG

541 TGGAAGTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA

601 GGACTCTACT CCCTCAGCAG CGTGCTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC

661 TACATCTGCA ACGTGAATCA CAAGCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC

721 AAATCTTGTG ACAAAGTCA CACATGCTGT GTCGAGTGTG CACCGTGTCC AGCACCAGAG

781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTGTTGGGA GACCAAGATG

841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG

901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT

961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT

1021 AAGGAGCGCT ACCTGTTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC

1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC

1141 AGGTTCTTCT CCCGGTTCAC AGAGGTCAGG GAGTTTGCCA TTGTTCCCTT GCATGCGGCC

1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG

1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GCGGACTTCA ATGCGGGCTG CAGCTATGTG

1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC

1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT

1441 GCAGGGATGC TGCTCCGAGG GGCCGTGTTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG

1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG

1561 GTGATGCTGA AGGGGGGCGG ACCCAAAAAG AAGCGCAAGG TTTGA

File : PAS106.DNA  
 Range : 1 - 1596 Mode : Normal  
 Codon Table : Universal

FIGURE 18(D)

	9			18			27			36			45			54		
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
	63			72			81			90			99			108		
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	117			126			135			144			153			162		
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
	171			180			189			198			207			216		
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	225			234			243			252			261			270		
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	279			288			297			306			315			324		
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
	333			342			351			360			369			378		
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
	387			396			405			414			423			432		
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	441			450			459			468			477			486		
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
	495			504			513			522			531			540		
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	549			558			567			576			585			594		
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

603			612			621			630			639			648		
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
657			666			675			684			693			702		
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K
711			720			729			738			747			756		
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	TGT	GTG	GAG	TGC	CCA	CCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	E	P	K	S	C	D	K	T	H	T	C	C	V	E	C	P	P
765			774			783			792			801			810		
TGC	CCA	GCA	CCT	GAA	GGG	AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
C	P	A	P	E	G	S	G	G	L	K	I	A	A	F	N	I	Q
819			828			837			846			855			864		
ACA	TTT	GGG	GAG	ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	F	G	E	T	K	M	S	N	A	T	L	V	S	Y	I	V	Q
873			882			891			900			909			918		
ATC	CTG	AGC	CGC	TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
I	L	S	R	Y	D	I	A	L	V	Q	E	V	R	D	S	H	L
927			936			945			954			963			972		
ACT	GCC	GTG	GGG	AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
T	A	V	G	K	L	L	D	N	L	N	Q	D	A	P	D	T	Y
981			990			999			1008			1017			1026		
CAC	TAC	GTG	GTC	AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
H	Y	V	V	S	E	P	L	G	R	N	S	Y	K	E	R	Y	L
1035			1044			1053			1062			1071			1080		
TTC	GTG	TAC	AGG	CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	V	Y	R	P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D
1089			1098			1107			1116			1125			1134		
GGC	TGC	GAG	CCC	TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	C	E	P	C	G	N	D	T	F	N	R	E	P	A	I	V	R
1143			1152			1161			1170			1179			1188		
TTC	TTC	TCC	CGG	TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	F	S	R	F	T	E	V	R	E	F	A	I	V	P	L	H	A
1197			1206			1215			1224			1233			1242		

GCC	CCG	GGG	GAC	CTA	GTA	GCC	GAG	ATC	GAC	GCT	CTC	TAT	CTC	GTC	TAC	CTG	GAT
A	P	G	D	A	V	A	E	I	D	A	L	Y	D	V	Y	L	D

1251	1260	1269	1278	1287	1296
GTC	CAA	GAG	AAA	TGG	GGC
TTC	AAT	GCG	GAC	ATG	TTG
V	Q	E	K	W	G

1305	1314	1323	1332	1341	1350
GGC	TGC	AGC	TAT	GTG	AGA
TCC	CAG	TGG	TCA	TCC	ATC
G	C	S	Y	V	R

1359	1368	1377	1386	1395	1404
CCC	ACC	TTC	CAG	TGG	CTG
ATC	CCC	GAC	AGC	GCT	GAC
P	T	F	Q	W	L

1413	1422	1431	1440	1449	1458
CAC	TGT	GCC	TAT	GAC	AGG
ATC	GTG	GTT	GCA	GGG	ATG
H	C	A	Y	D	R

1467	1476	1485	1494	1503	1512
GTT	CCC	GAC	TCG	GCT	CTT
CCC	TTT	AAC	TTC	CAG	GCT
V	P	D	S	A	L

1521	1530	1539	1548	1557	1566
CAA	CTG	GCC	CAA	GCC	ATC
AGT	GAC	CAC	TAT	CCA	GTG
Q	L	A	Q	A	I

1575	1584	1593
GGC	GGA	CCC
AAA	AAG	AAG
G	G	P

## FIGURE 19

(A) pAS107

LOCUS PAS107.DNA 1590 bp mRNA PRI 06-MAR-1995  
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40 NLS(pAS107)  
 ACCESSION  
 NID  
 KEYWORDS DNase I.  
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f  
 MHDNASE1.dna)  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.  
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis  
 sputum  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)  
 MEDLINE 91067672  
 BASE COUNT 354 a 474 c 448 g 314 t  
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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGTCCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAAC TCACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG
781 AAGATCGCAG CTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGAG
1261 GACGTCAATG TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCAGTG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

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//

↳ NLS

Figure 19 (B)

LOCUS FDDNASE107 1590 BP SS-DNA SYN 25-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -  
 FEATURES Location/Qualifiers  
   frag join(1..>720,<793..1590)  
     /note="1 to 1590 of PAS107.dna [Split]"  
   frag 721..792  
     /note="1 to 72 of 103/107linker"  
   frag join(721..>771,<772..792)  
     /note="1 to 78 of 102linker [Split]"  
 BASE COUNT 354 A 473 C 448 G 315 T 0 OTHER  
 ORIGIN -

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1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAATCTA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGAAGTCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAAGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGAG
1261 GACGTCAATG TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCAGTG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
1561 GGCGGACCCA AAAAGAAGCG CAAGTTTGA

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LOCUS FDDNASE107 1599 BP SS-DNA SYN 29-AUG-2000  
 DEFINITION -  
 ACCESSION -  
 KEYWORDS -  
 SOURCE -

FEATURES Location/Qualifiers  
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 /note="1 to 1590 of FdDNase107correct"  
 frag join(10..>729,<802..1599)  
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 frag 730..801  
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BASE COUNT 355 A 479 C 450 G 315 T 0 OTHER

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 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG  
 121 AAGGTGTCTT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC  
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT  
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 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA  
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA  
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG  
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG  
 541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA  
 601 GGAATCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC  
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC  
 721 AAATCTTGTG ACAAACCTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG  
 781 GGCGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTTG GGGAGACCAA GATGTCCAAT  
 841 GCCACCCCTG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG  
 901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAGCTGC TGGACAACCT CAATCAGGAC  
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 1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTGAGGTTT  
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 1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG  
 1261 GGCTTGAGAG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC  
 1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC  
 1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTGCAGGG  
 1441 ATGCTGCTCC GAGGGGCCGT TGTTCCCGAC TCGGCTCTTC CTTTAACTT CCAGGCTGCC  
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File : PAS107.DNA  
 Range : 1 - 590 Mode : Normal  
 Codon Table : Universal

FIGURE 19 (0)

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M G W S C I I L F L V A T A T G V H						
63	72	81	90	99	108	
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA						
S Q V Q L V Q S G A E V K K P G A S						
117	126	135	144	153	162	
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG						
V K V S C K A S G Y T F S A Y W I E						
171	180	189	198	207	216	
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT						
W V R Q A P G K G L E W V G E I L P						
225	234	243	252	261	270	
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT						
G S N N S R Y N E K F K G R V T V T						
279	288	297	306	315	324	
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG						
R D T S T N T A Y M E L S S L R S E						
333	342	351	360	369	378	
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC						
D T A V Y Y C A R S Y D F A W F A Y						
387	396	405	414	423	432	
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG						
W G Q G T L V T V S S A S T K G P S						
441	450	459	468	477	486	
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG						
V F P L A P S S K S T S G G T A A L						
495	504	513	522	531	540	
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA						
G C L V K D Y F P E P V T V S W N S						
549	558	567	576	585	594	
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA						
G A L T S G V H T F P A V L Q S S G						

603					612			621			630			639			648		
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG		
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L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q		
657					666			675			684			693			702		
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K		
711					720			729			738			747			756		
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	TGT	GTG	GAG	TGC	CCA	CCG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
V	E	P	K	S	C	D	K	T	H	T	C	C	V	E	C	P	P		
765					774			783			792			801			810		
TGC	CCA	GCA	CCT	GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
C	P	A	P	E	G	G	L	K	I	A	A	F	N	I	Q	T	F		
819					828			837			846			855			864		
GGG	GAG	ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
G	E	T	K	M	S	N	A	T	L	V	S	Y	I	V	Q	I	L		
873					882			891			900			909			918		
AGC	CGC	TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC		
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S	R	Y	D	I	A	L	V	Q	E	V	R	D	S	H	L	T	A		
927					936			945			954			963			972		
GTG	GGG	AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC		
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V	G	K	L	L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y		
981					990			999			1008			1017			1026		
GTG	GTC	AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG		
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V	V	S	E	P	L	G	R	N	S	Y	K	E	R	Y	L	F	V		
1035					1044			1053			1062			1071			1080		
TAC	AGG	CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC		
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Y	R	P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C		
1089					1098			1107			1116			1125			1134		
GAG	CCC	TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
E	P	C	G	N	D	T	F	N	R	E	P	A	I	V	R	F	F		
1143					1152			1161			1170			1179			1188		
TCC	CGG	TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG		
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
S	R	F	T	E	V	R	E	F	A	I	V	P	L	H	A	A	P		
1197					1206			1215			1224			1233			1242		

GGG GAC GCA GTA GAG ATC GAC GCT CTC TAT GAC GTC CTG GAT GTC CAA  
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G D A V A E I D A L Y D V Y L D V Q  
  
1251 1260 1269 1278 1287 1296  
GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC  
-----  
E K W G L E D V M L M G D F N A G C  
  
1305 1314 1323 1332 1341 1350  
AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC  
-----  
S Y V R P S Q W S S I R L W T S P T  
  
1359 1368 1377 1386 1395 1404  
TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT  
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F Q W L I P D S A D T T A T P T H C  
  
1413 1422 1431 1440 1449 1458  
GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC  
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A Y D R I V V A G M L L R G A V V P  
  
1467 1476 1485 1494 1503 1512  
GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG  
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D S A L P F N F Q A A Y G L S D Q L  
  
1521 1530 1539 1548 1557 1566  
GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA  
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A Q A I S D H Y P V E V M L K G G G  
  
1575 1584  
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P K K K R K V \*

Fig 20 Mammalian expression of humanised HMFG1-DNase constructs

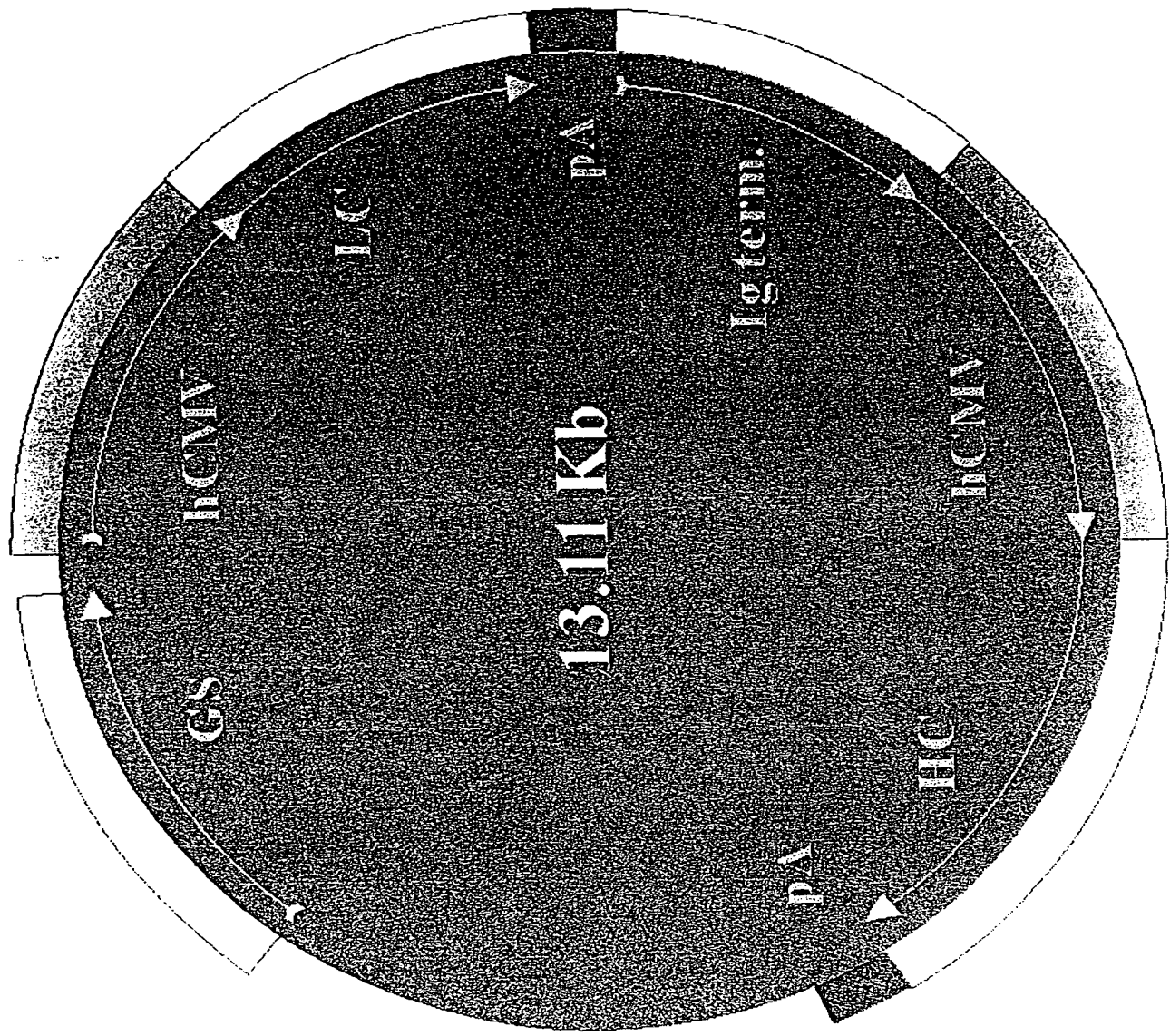
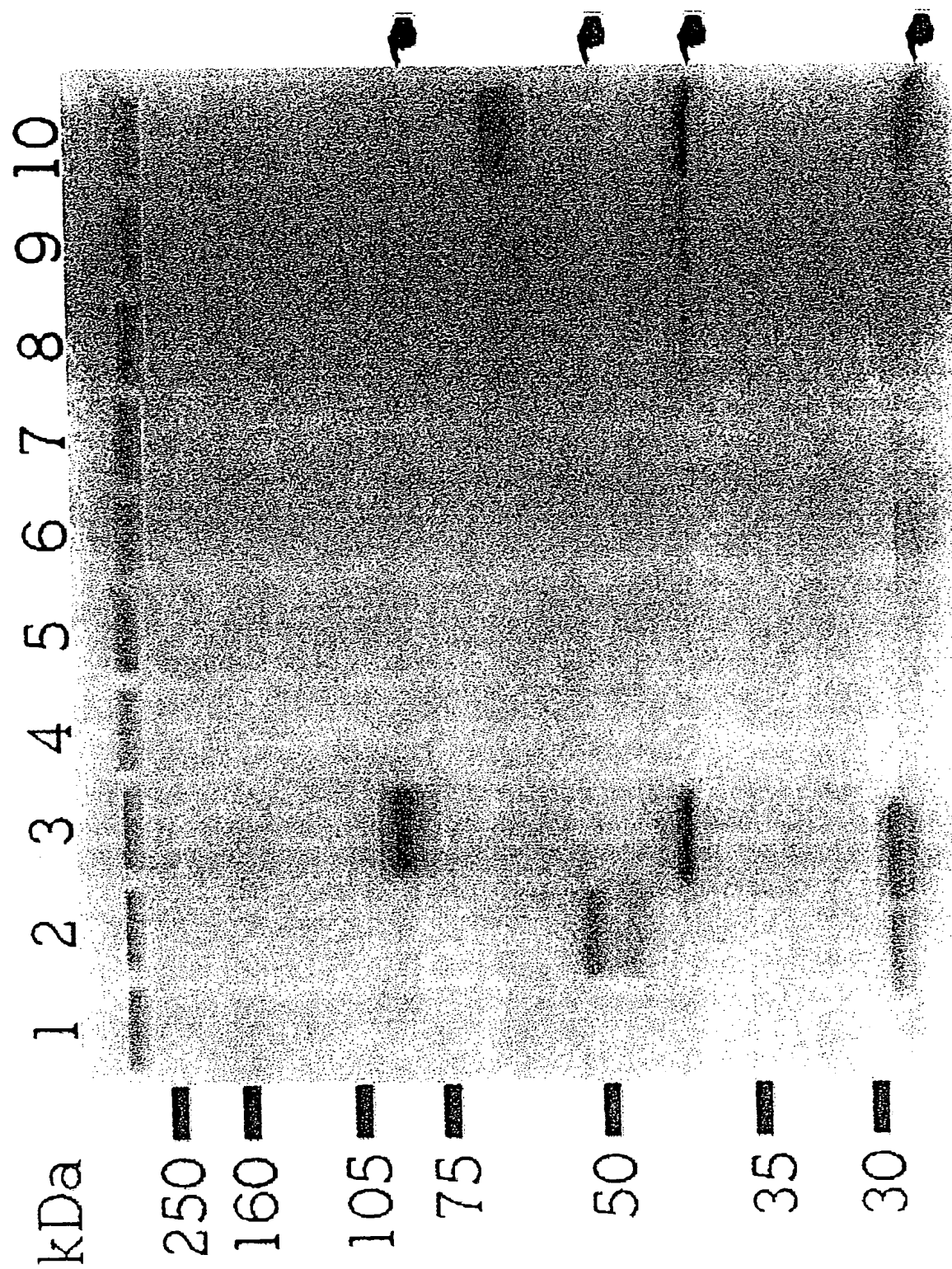
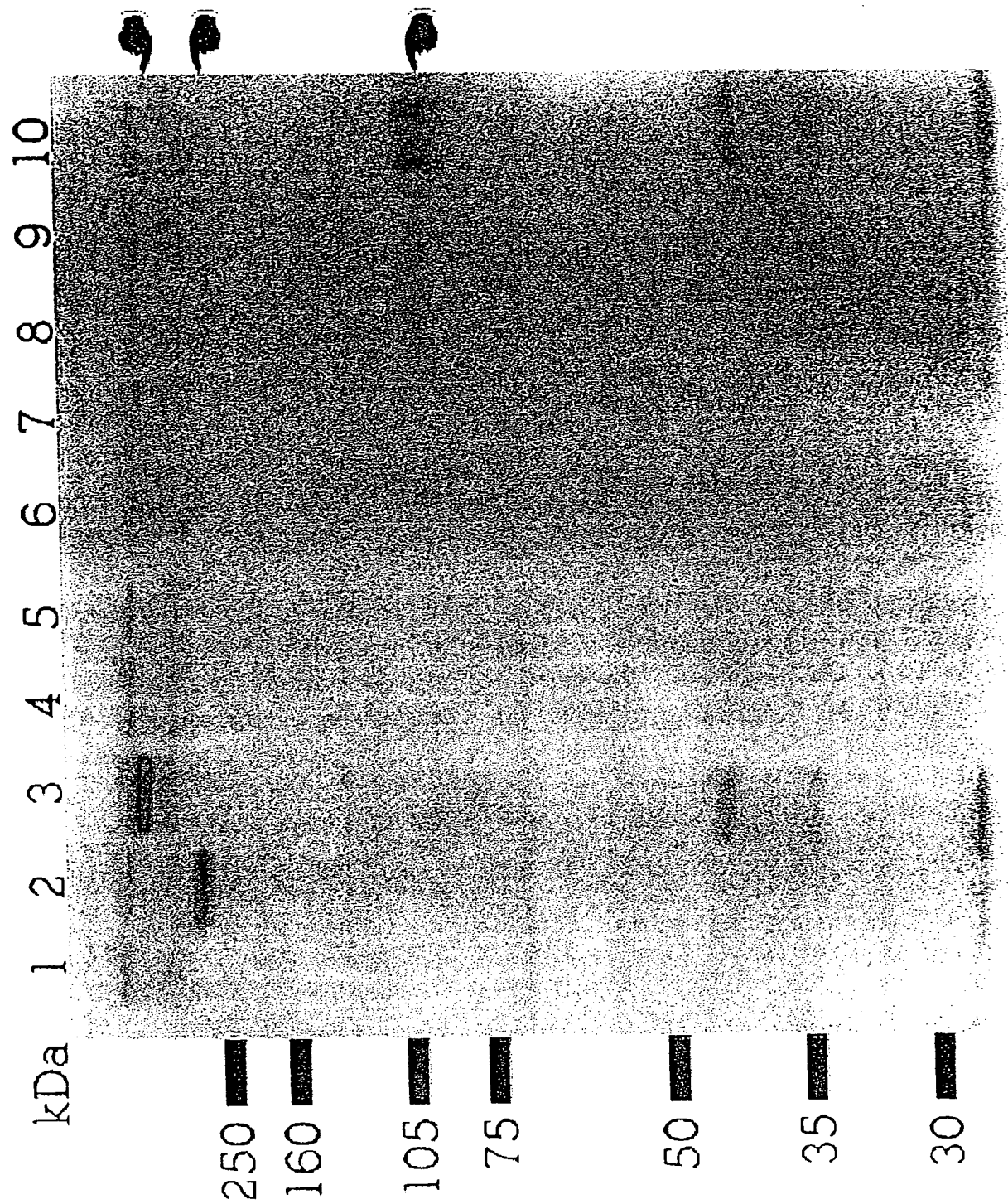


Fig 2(A) Immuno-precipitation of metabolically labelled transient transfectants



8% SDS-PAGE reducing gel

Fig 21 (3) Immuno-precipitation of metabolically labelled transient transfectants



100% CMC PAGE non-reducing gel

Fig 21 Immuno-precipitation of metabolically labelled transient transfectants

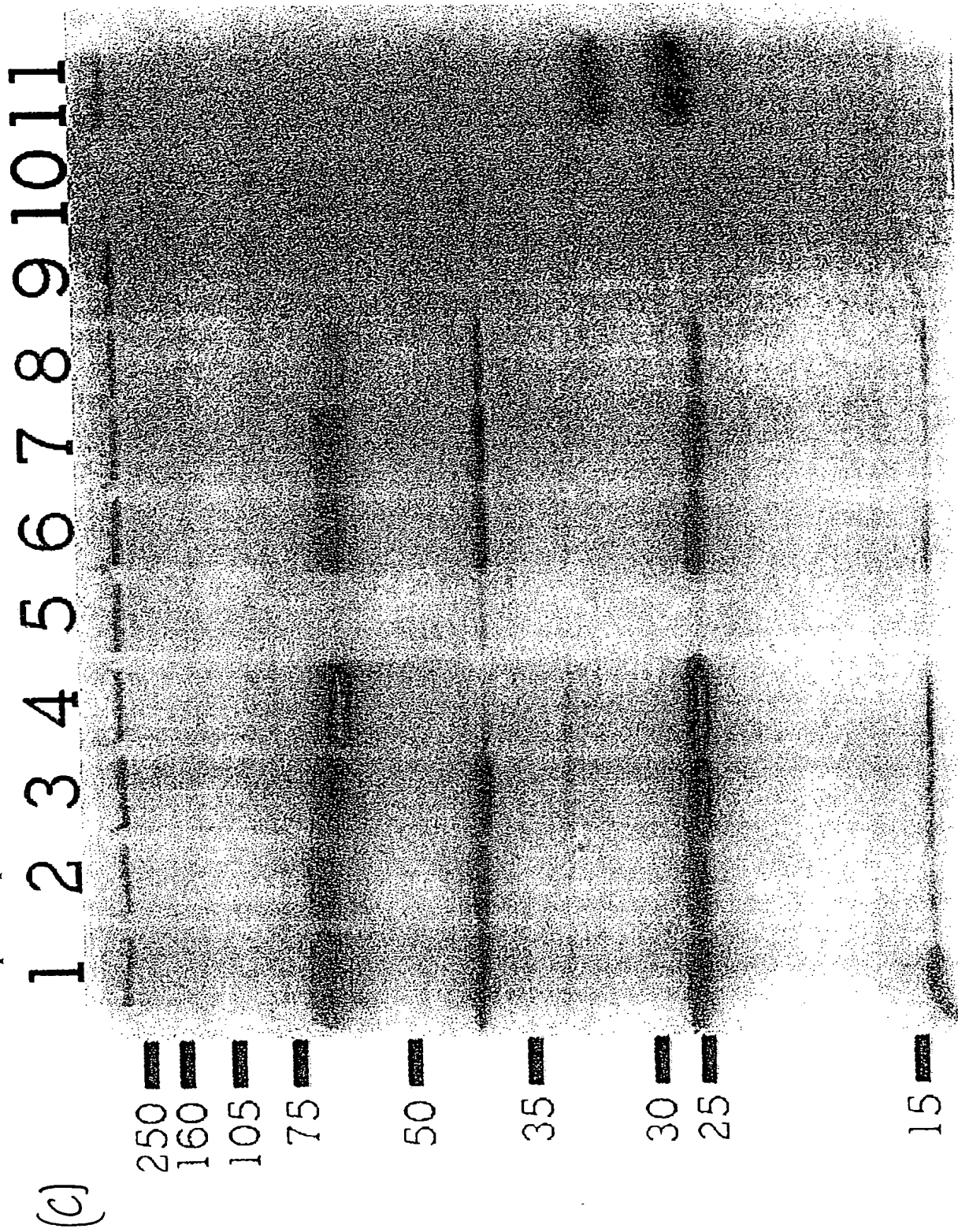


Fig 2/1 Immuno-precipitation of metabolically labelled transient transfectants

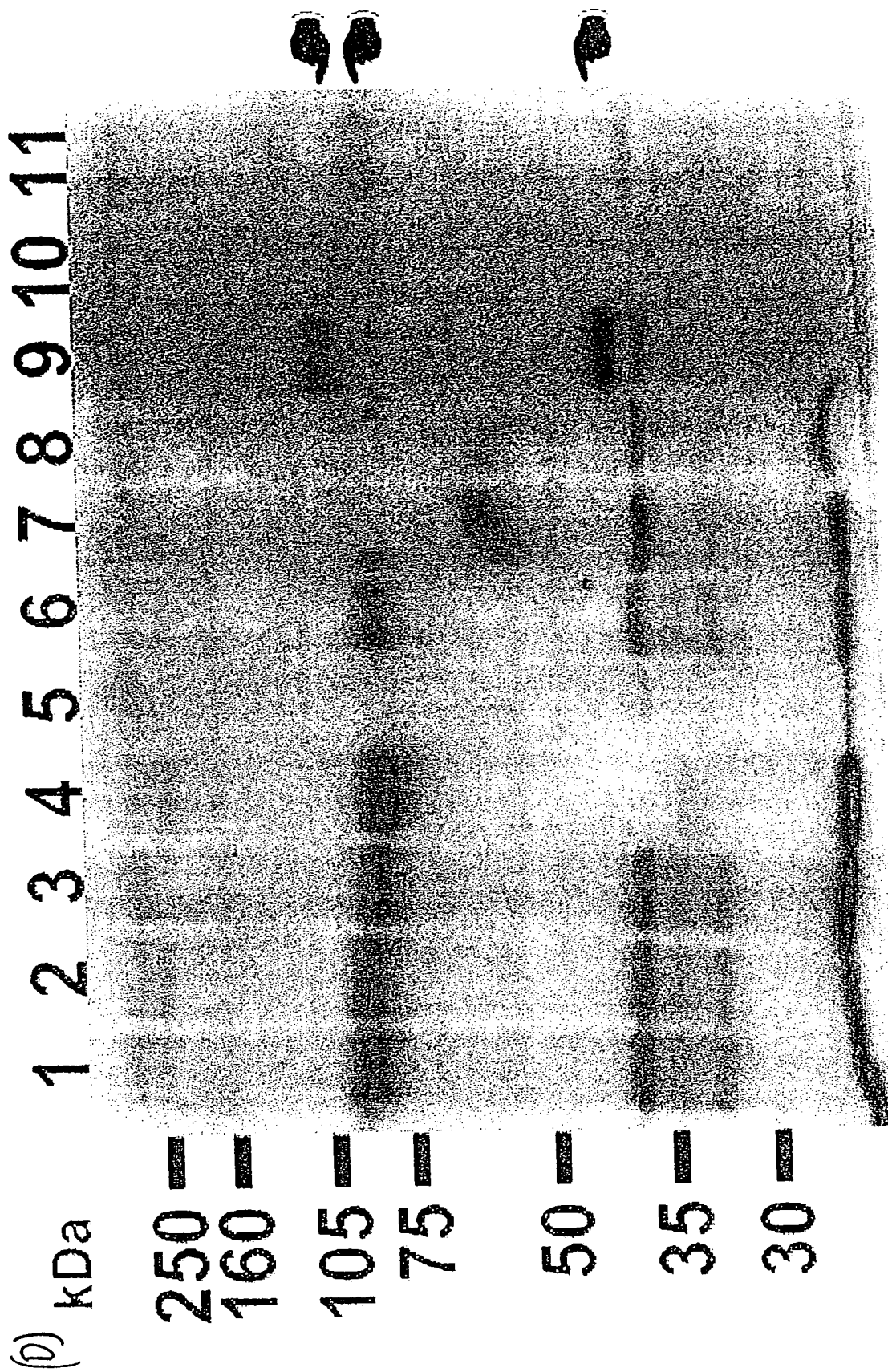


Fig 22

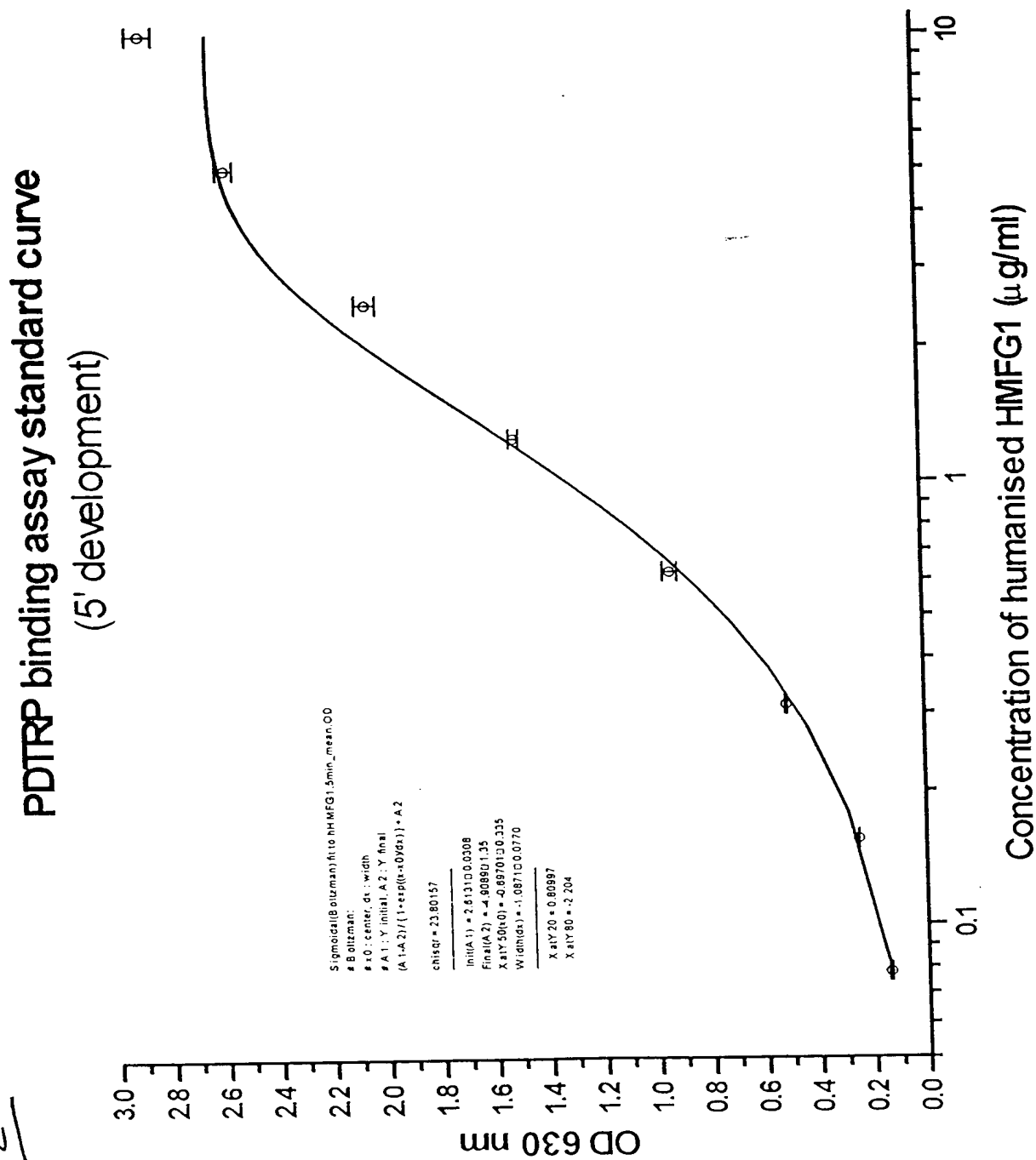


Fig 23

Corrected bovine DNase I standard curves  
at various time points

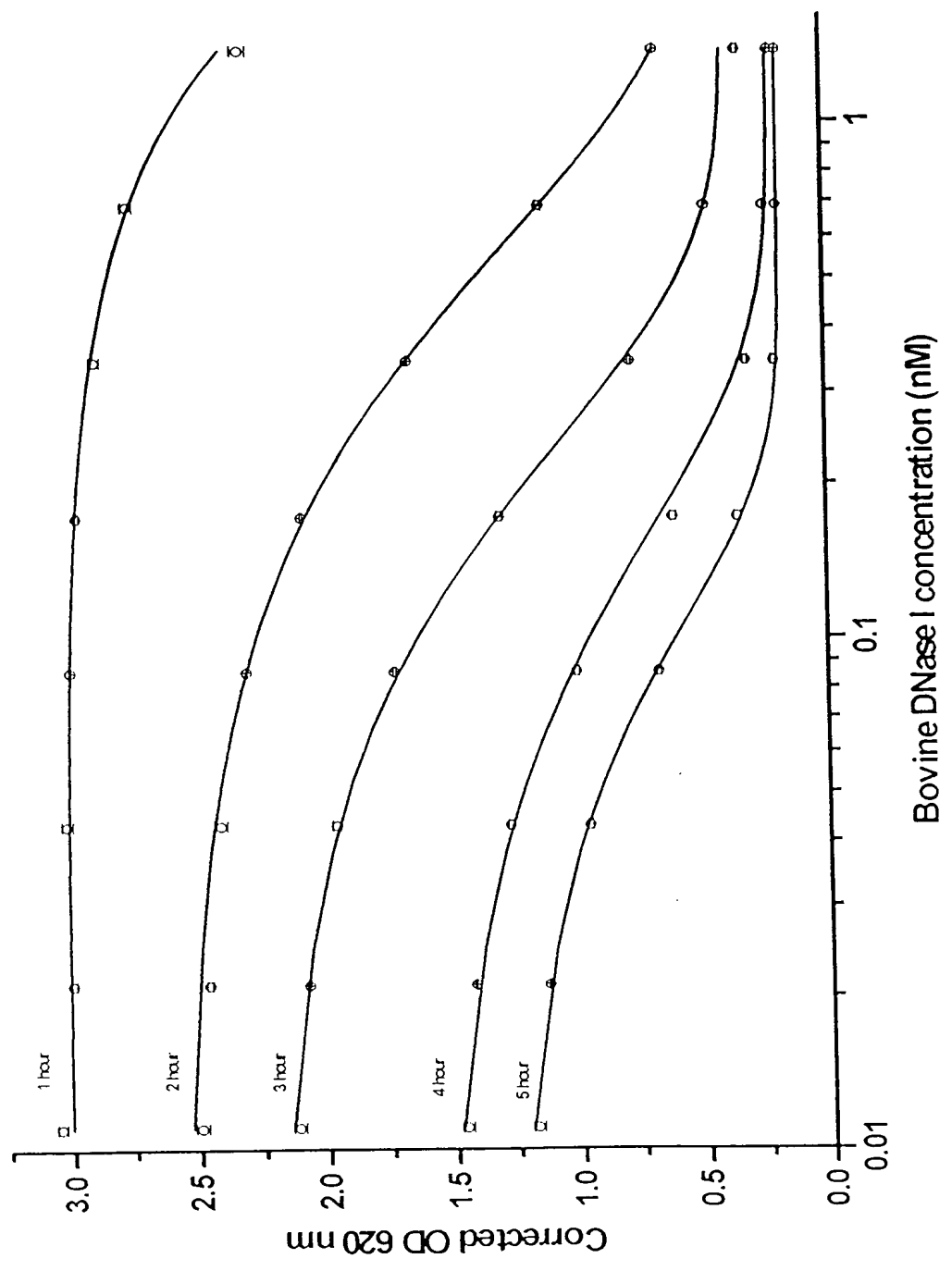


FIG 24

Corrected DNase I activity in transiently expressed  
humanised human HMFG1-human DNase I constructs

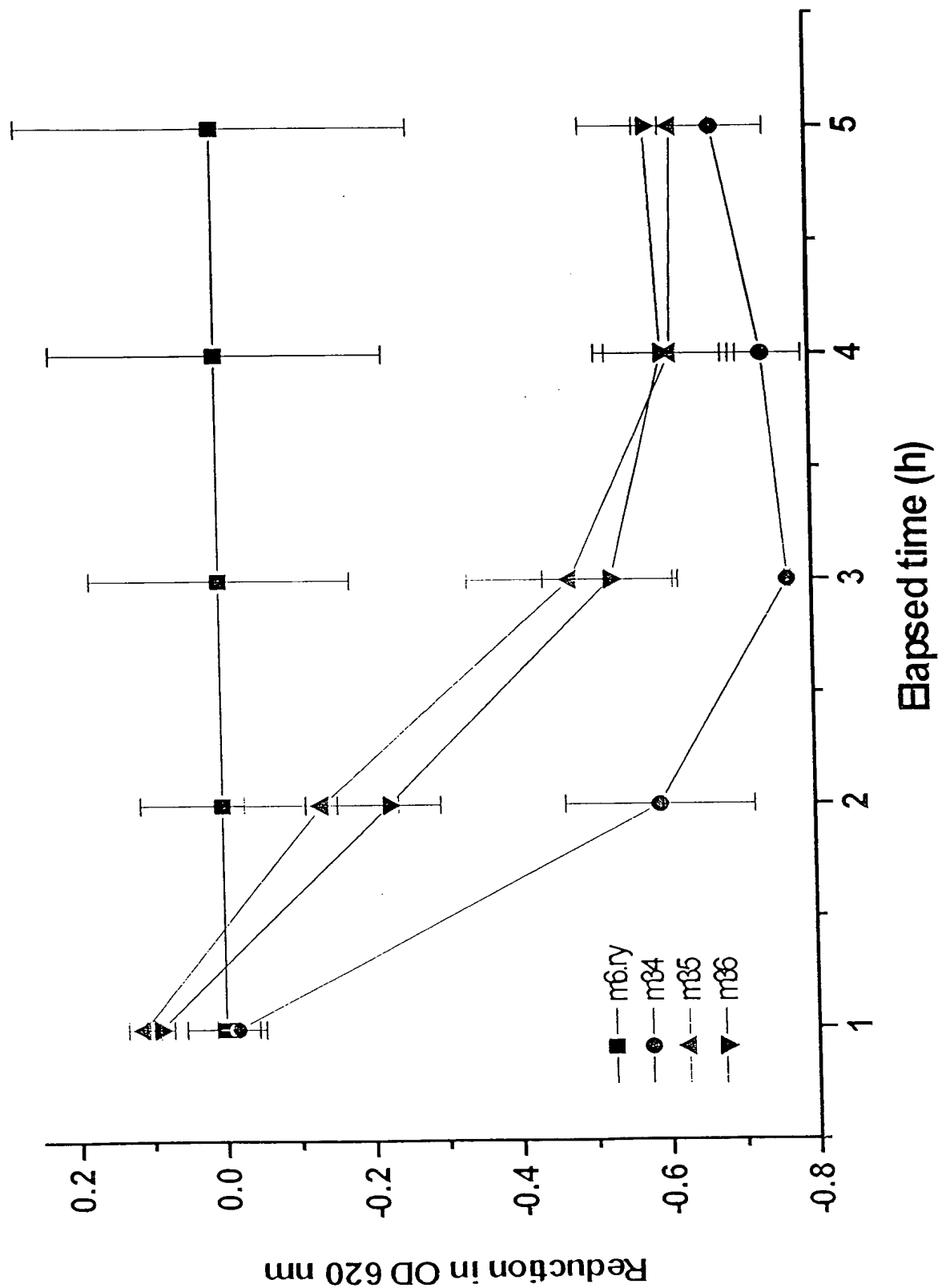


Fig 25

Corrected DNase I activity in transiently expressed  
humanised HMFG1 F(ab')<sub>2</sub>-human DNase I fusions

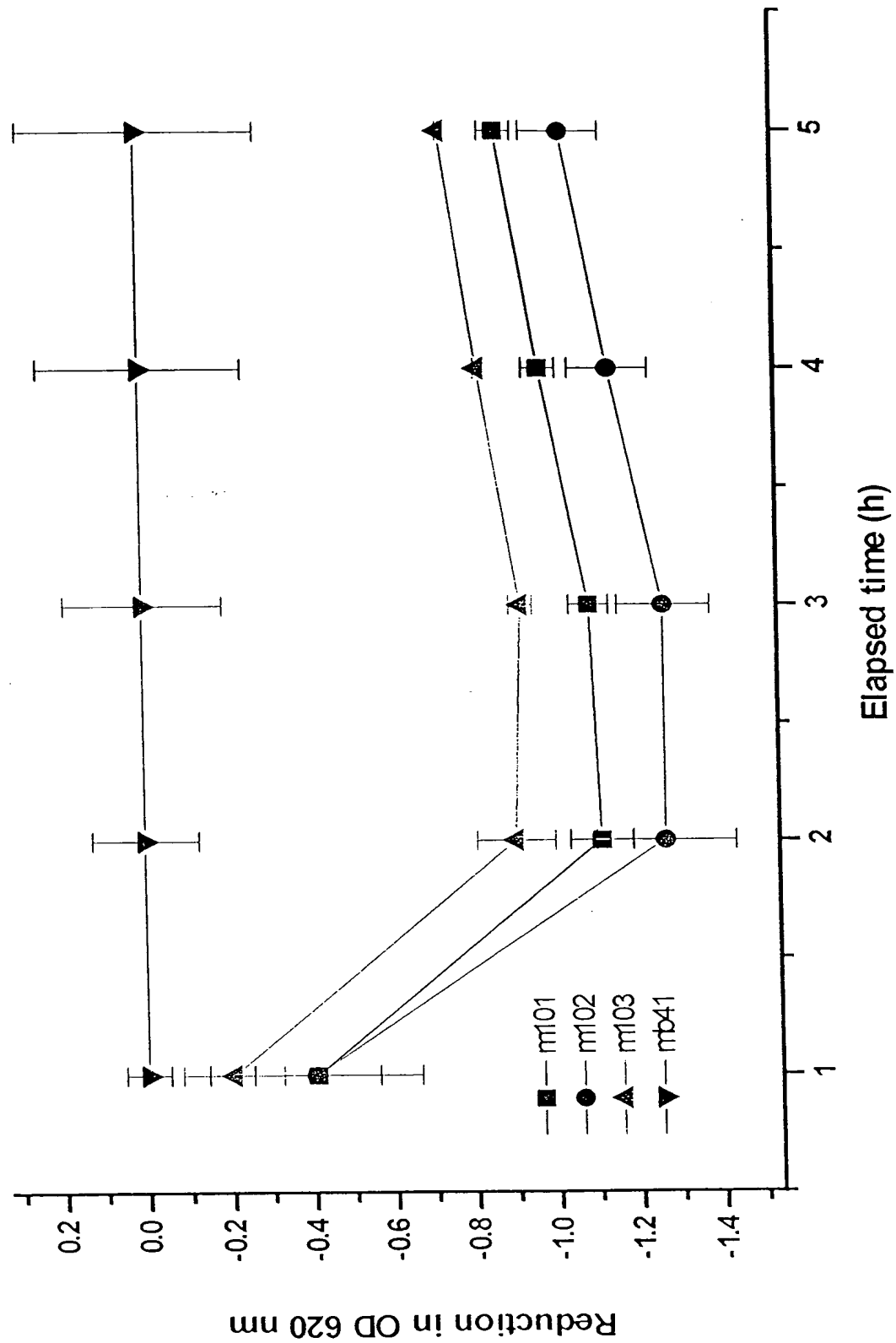
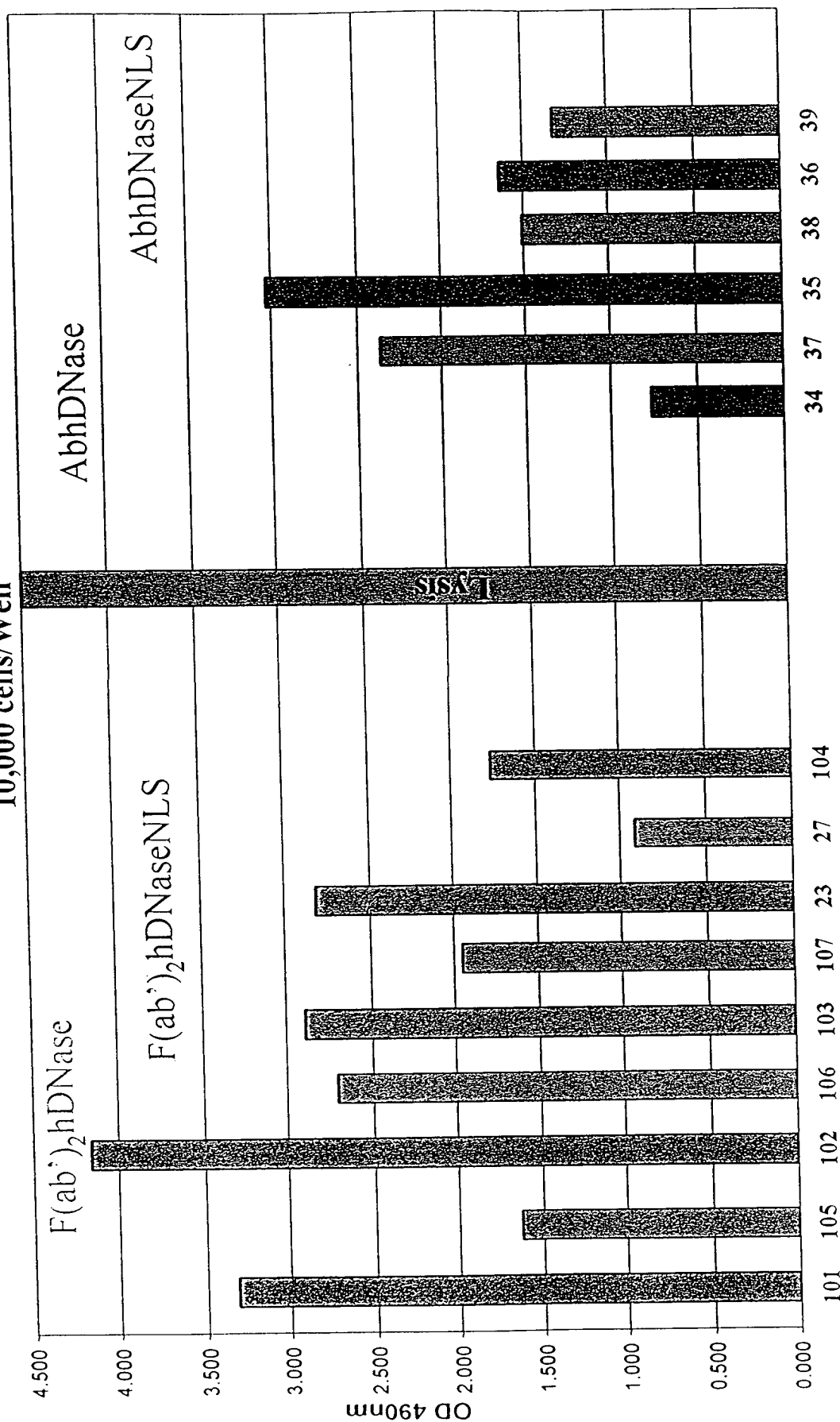


FIG. 26

Cytotoxicity Assay

10,000 cells/Well



0.097 µg/ml of each construct

Fig 27

MCF7 cells killed after 1h incubation with 1.35 ng of sample

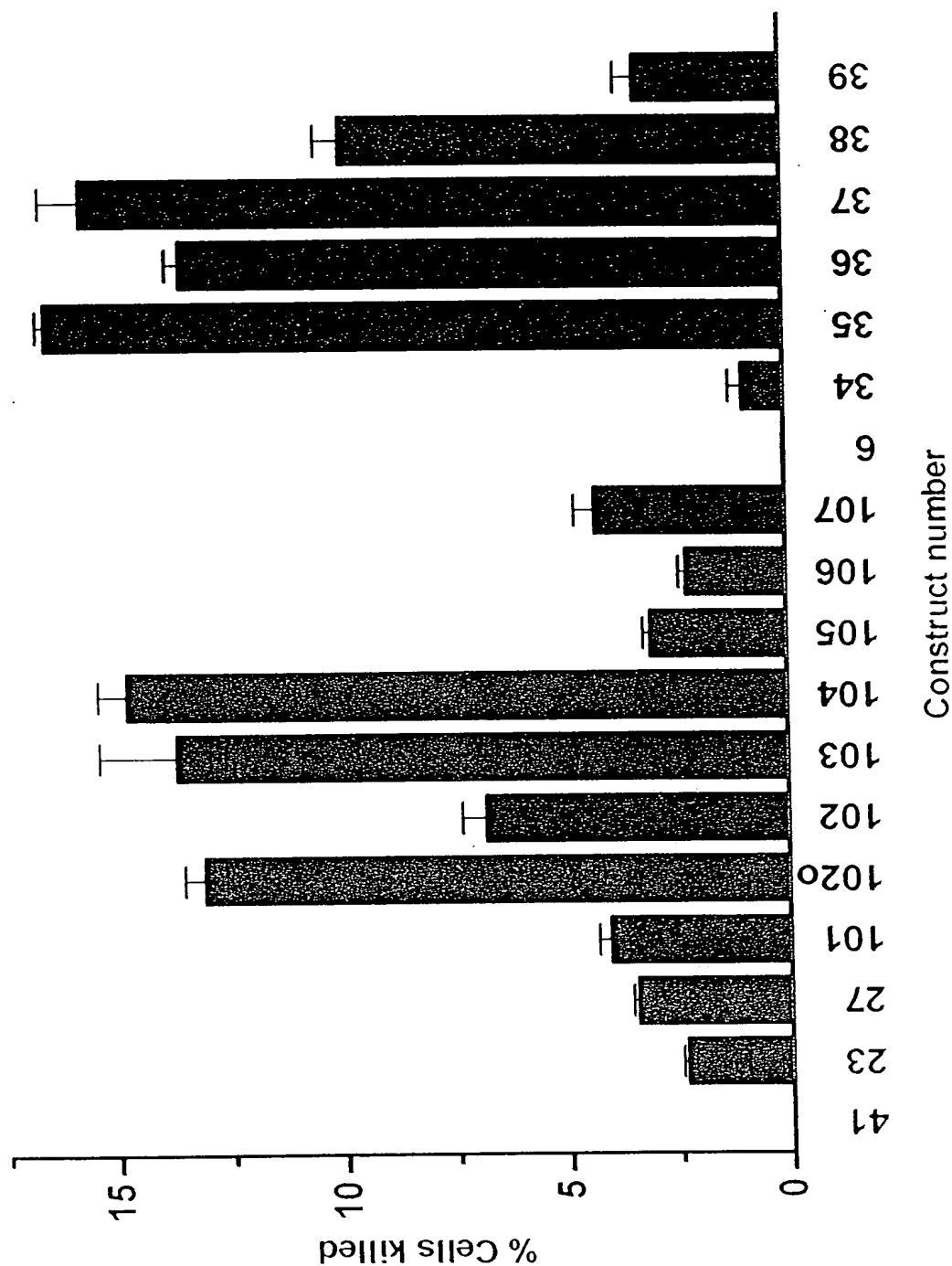


Figure 28

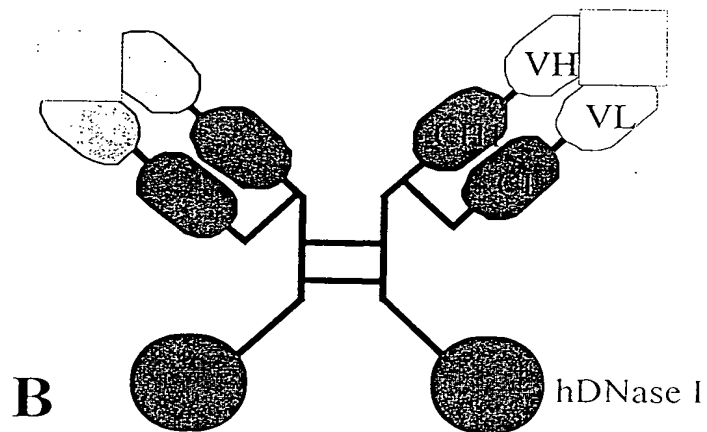
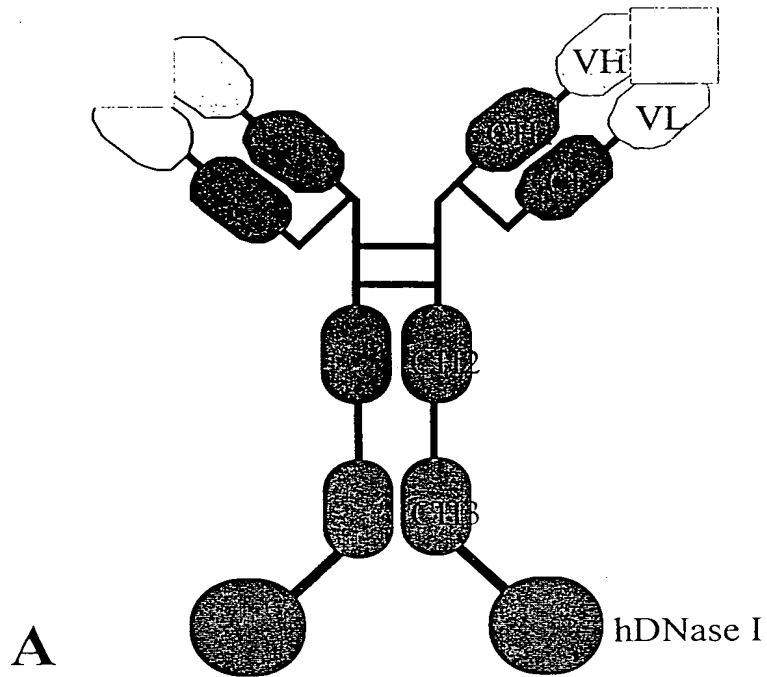
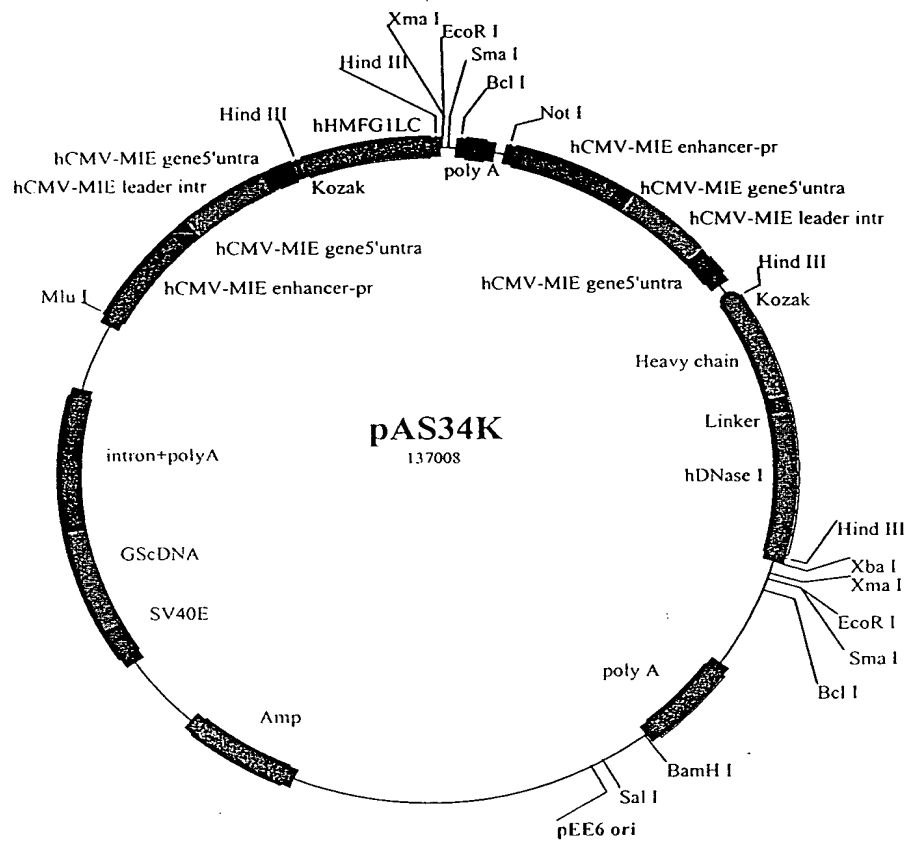
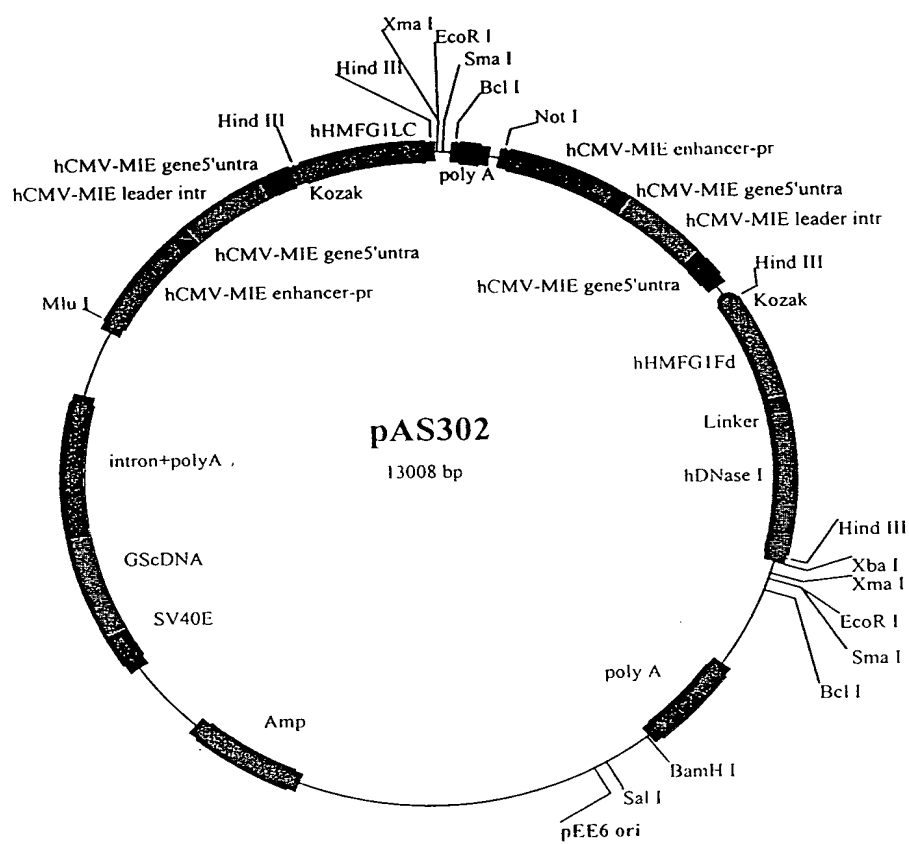


Figure 29



Ab-DNase

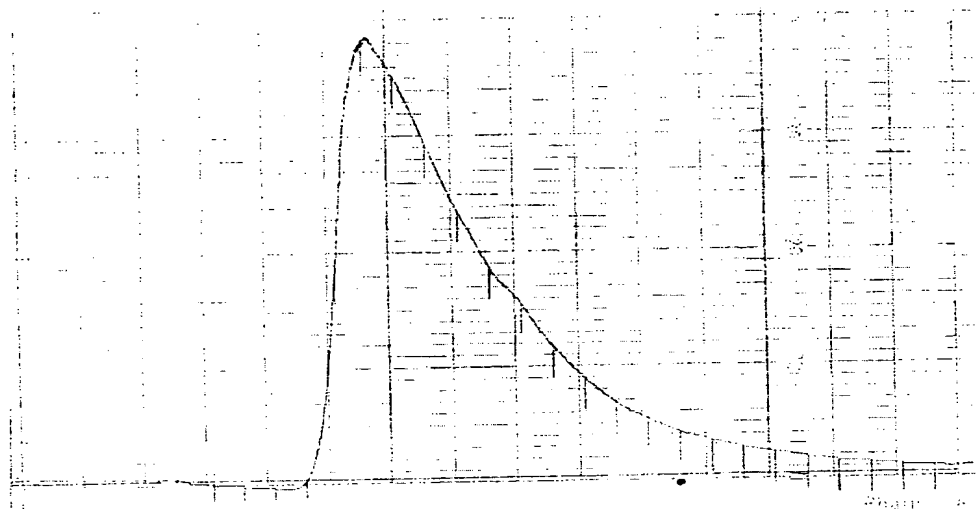
Figure 30



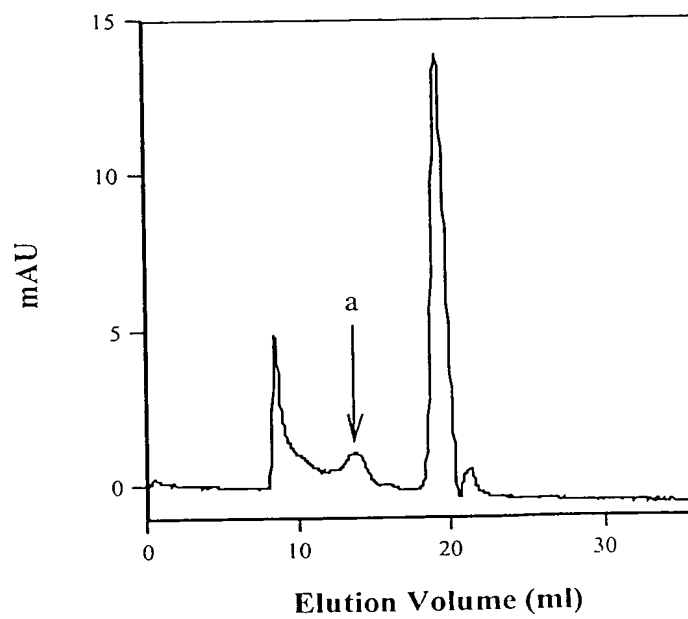
**Fab-DNase**

Figure 31

A

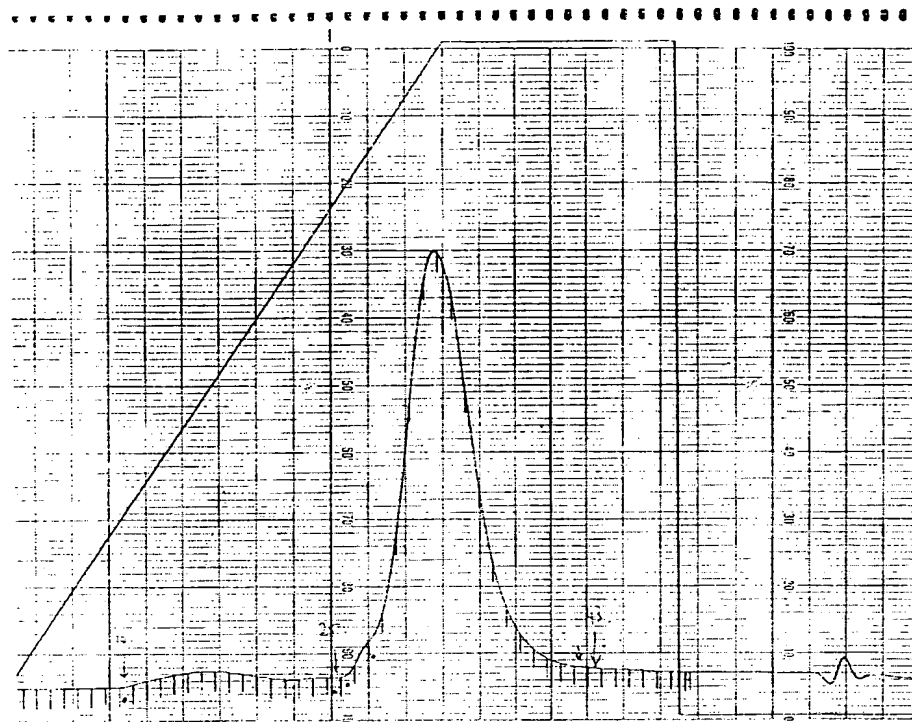


B



**A**

Figure 32



**B**

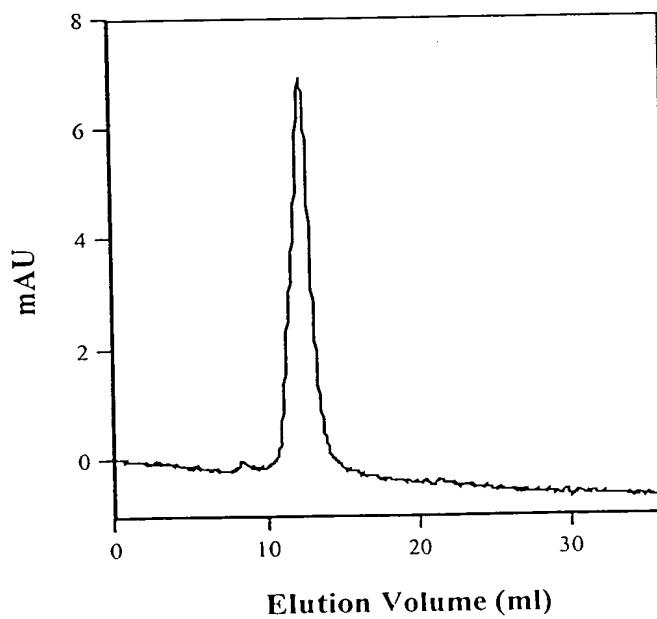


Figure 33

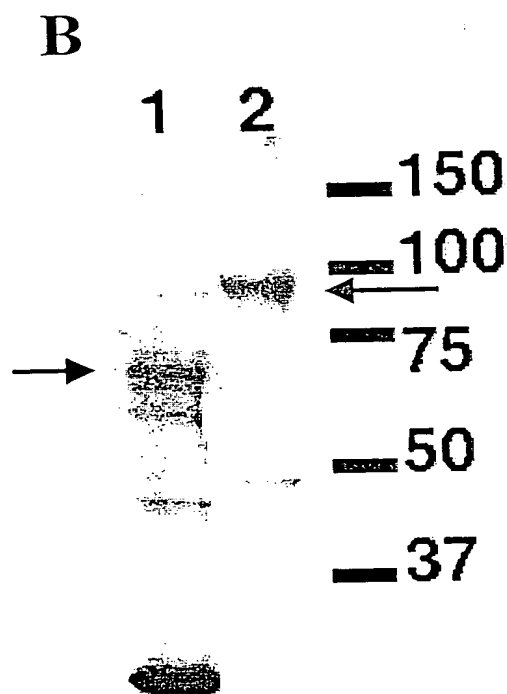
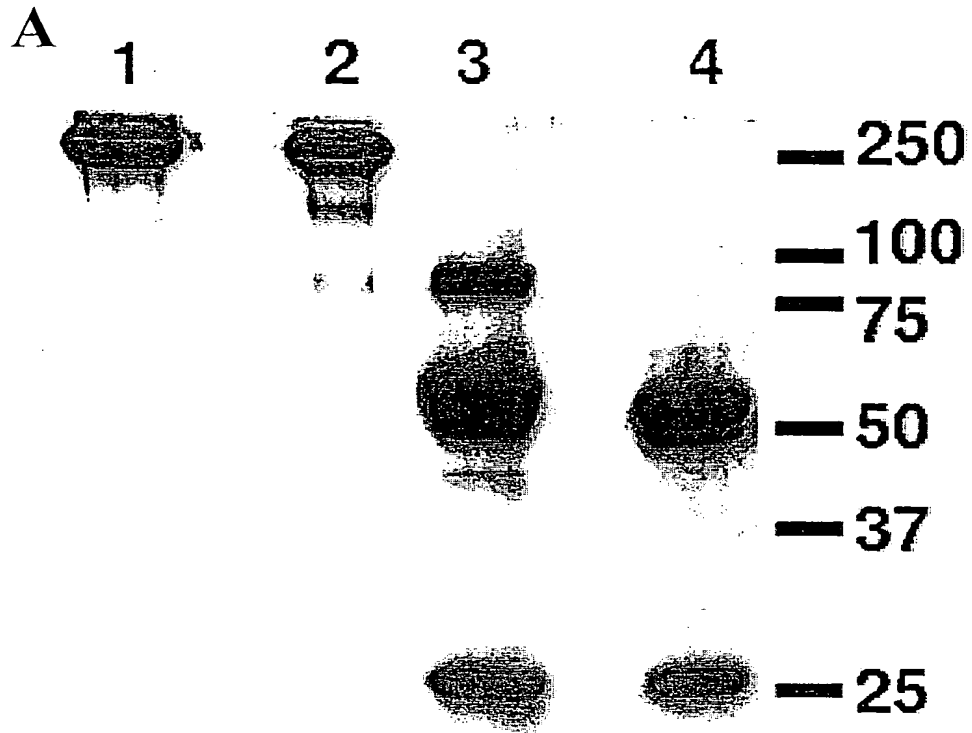
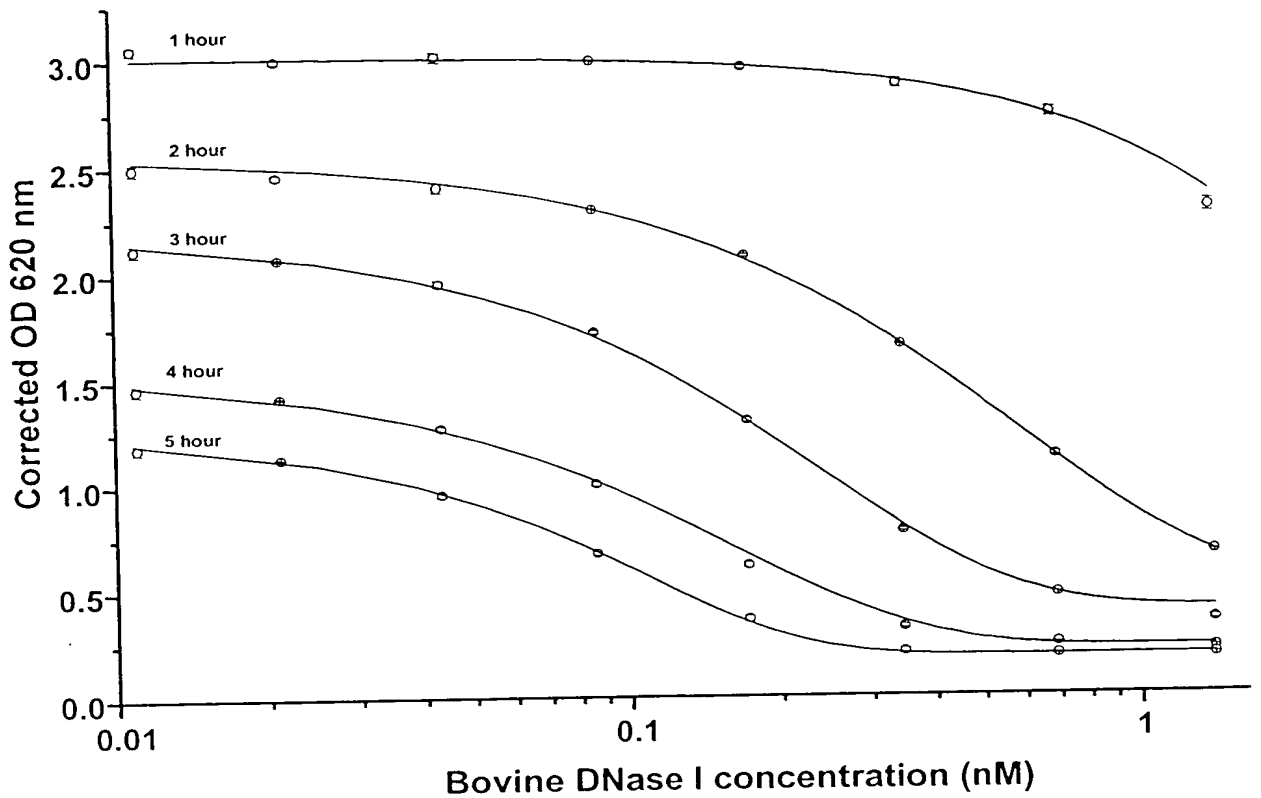


Figure 34

## Bovine DNase I standard curves at various time points



A

Figure 34 – cont.

**B**

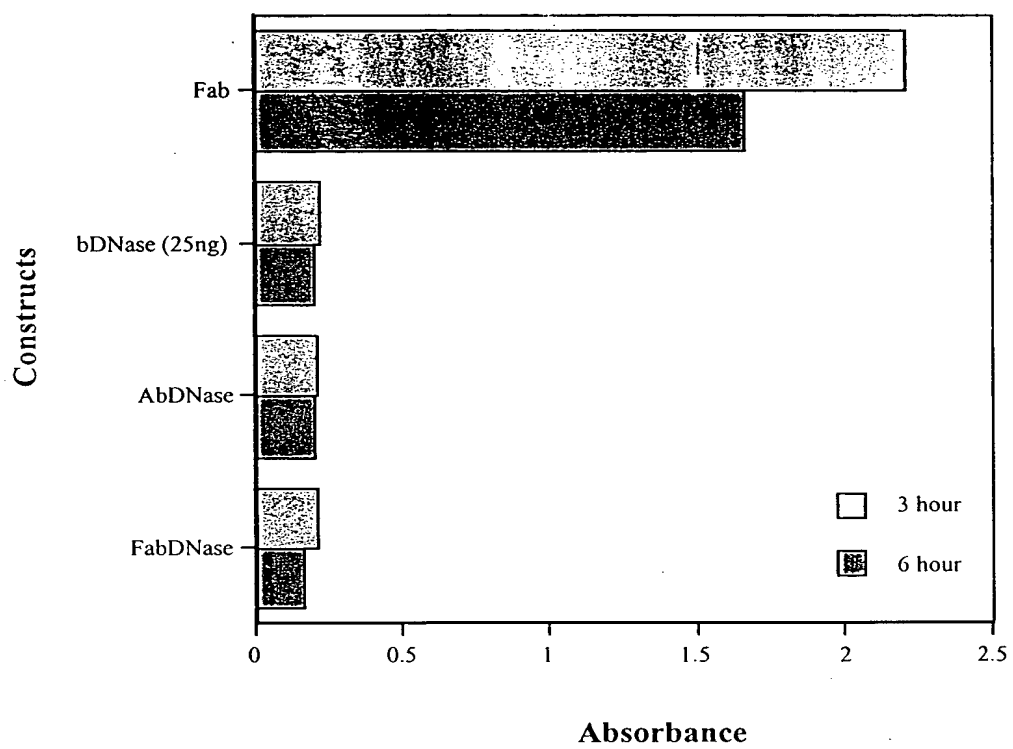


Figure 35

A

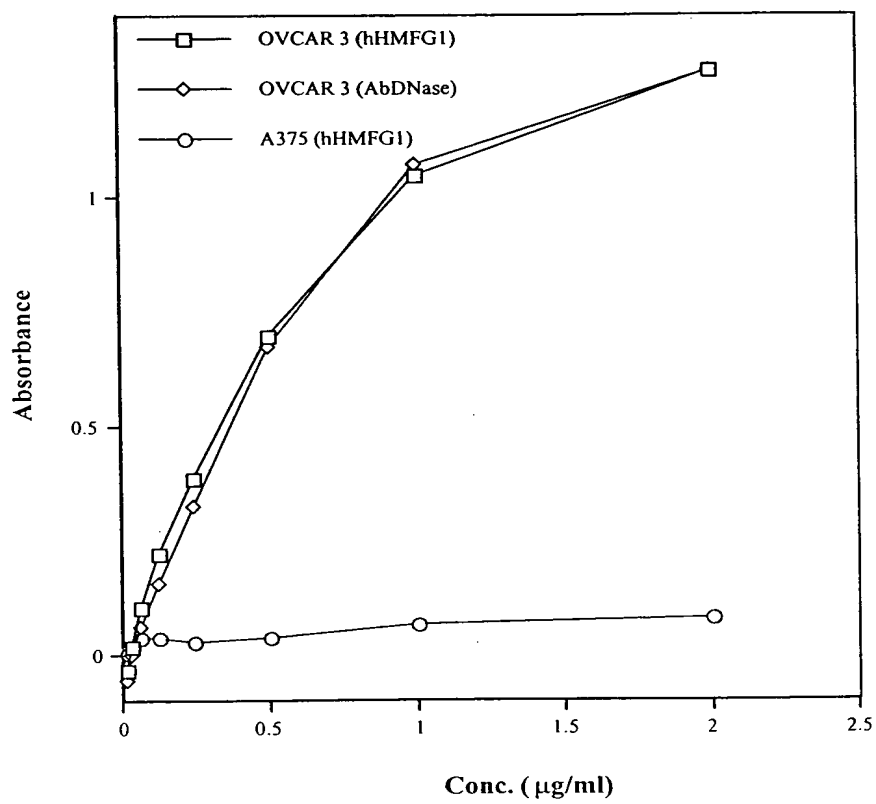
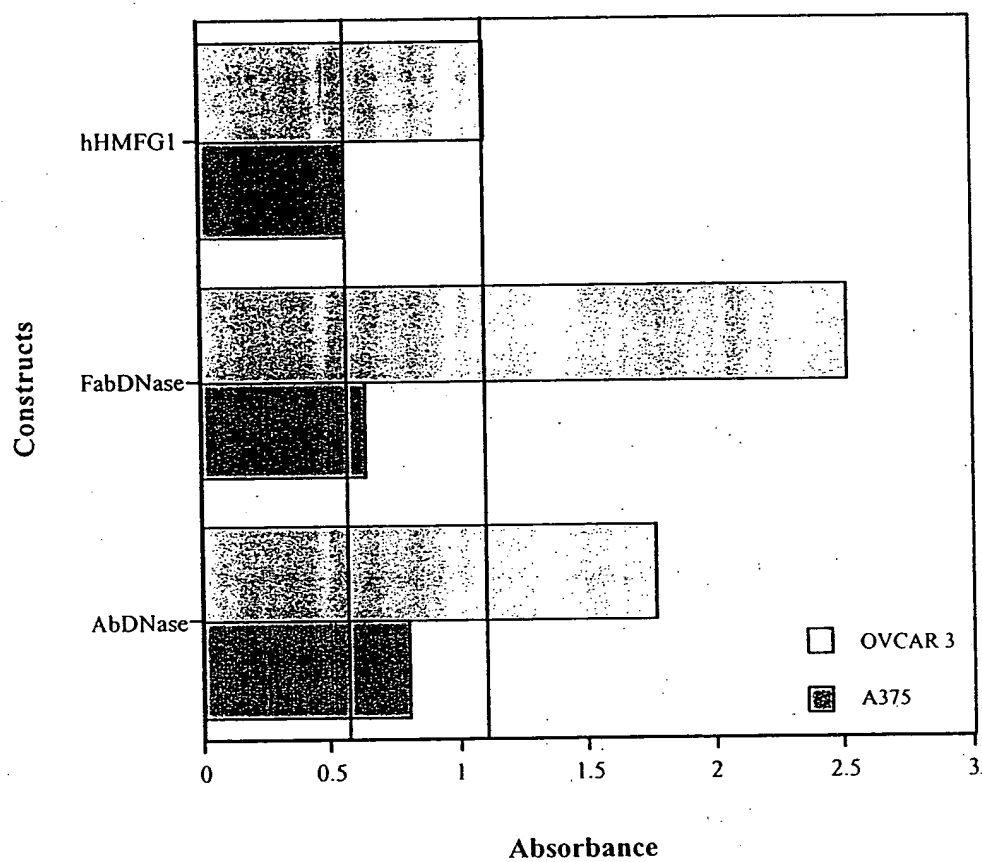


Figure 35 – cont.

**B**



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